INTERFERON-BETA FUSION PROTEINS AND USES

RELATED APPLICATIONS

This is a continuation of PCT/US99/24200, filed on October 15, 1999 as a continuation-in-part of prior U.S. Provisional S.N. 60/104,491 filed October 16, 1998 and

5   U.S. Provisional S. N. 60/120,237 filed February 16, 1999. The teachings of the earlier-filed patent applications are incorporated herein by reference.

BACKGROUND OF THE INVENTION

Use of polypeptides and proteins for the systemic treatment of specific diseases is now well accepted in medical practice. The role that these substances play in therapy is so

10   important that many research activities are being directed towards the synthesis of large quantities by recombinant DNA technology. Many of these polypeptides are endogenous molecules which are very potent and specific in eliciting their biological actions.

A major factor limiting the usefulness of these proteinaceous substances for their intended application is that, when given parenterally, they are eliminated from the body

15   within a short time. This can occur as a result of metabolism by proteases or by clearance using normal pathways for protein elimination such as by filtration in the kidneys. The problems associated with these routes of administration of proteins are well known in the pharmaceutical industry, and various strategies are being used in attempts to solve them.

A peptide family, which has been the focus of much clinical work, and efforts to

20   improve its administration and bio-assimilation, is the interferons. Interferons have been tested in a variety of clinical disease states. The use of human interferon beta, one member of that family, is best established in the treatment of multiple sclerosis. Two forms of recombinant interferon beta, have recently been licensed in Europe and the U.S. for treatment of this disease. One form is interferon-beta-1a (trademarked, sold as AVONEX

25   ®, mfg. Biogen, Inc., Cambridge, MA) and hereinafter, "interferon- beta-1a" or "IFN-beta-1a" or "IFN-β-1a" or "interferon-β-1a", used interchangeably. The other form is interferon-beta-1b (trademarked and sold as BETASERON ®, Berlex, Richmond CA), hereinafter, "interferon-beta-1b". Interferon beta-1a is produced in mammalian cells using the natural human gene sequence and is glycosylated, whereas interferon beta-1b is

30   produced in E. coli bacteria using a modified human gene sequence that contains a

genetically engineered cysteine-to-serine substitution at amino acid position 17 and is non-glycosylated.

Previously, several of us have directly compared the relative *in vitro* potencies of interferon-beta-1a and interferon beta 1b in functional assays and showed that the specific

5   activity of interferon-beta-1a is approximately 10-fold greater than the specific activity of interferon-beta-1b (Runkel et al., 1998, Pharm. Res. 15: 641-649). From studies designed to identify the structural basis for these activity differences, we identified glycosylation as the only one of the known structural differences between the products that affected the specific activity. The effect of the carbohydrate was largely manifested through its

10   stabilizing role on structure. The stabilizing effect of the carbohydrate was evident in thermal denaturation experiments and SEC analysis. Lack of glycosylation was also correlated with an increase in aggregation and an increased sensitivity to thermal denaturation. Enzymatic removal of the carbohydrate from interferon-beta-1a with PNGase F caused extensive precipitation of the deglycosylated product.

15   These studies indicate that, despite the conservation in sequence between interferon-beta-1a and interferon-beta-1b, they are distinct biochemical entities and therefore much of what is known about interferon-beta-1b cannot be applied to interferon-beta-1a, and vice versa.

SUMMARY OF THE INVENTION

20   We have exploited the advantages of glycosylated interferon-beta relative to non-glycosylated forms. In particular, we have developed an interferon-beta-1a composition with increased activity relative to interferon-beta-1b and that also has the salutory properties of fusion proteins in general with no effective loss in activity as compared to interferon-beta-1a forms that are not fusion proteins. Thus, if modifications are made in

25   such a way that the products (interferon-beta 1a fusion proteins) retain all or most of their biological activities, the following properties may result: altered pharmacokinetics and pharmacodynamics leading to increased half-life and alterations in tissue distribution (e.g, ability to stay in the vasculature for longer periods of time) Such a formulation is a substantial advance in the pharmaceutical and medical arts and would make a significant

30   contribution to the management of various diseases in which interferon has some utility, such as multiple sclerosis, fibrosis, and other inflammatory or autoimmune diseases,

cancers, hepatitis and other viral diseases and diseases characterized by neovascularization. In particular, the ability to remain for longer periods of time in the vasculature allows the interferon-beta-1a to be used to inhibit angiogenesis and potentially to cross the blood-brain barrier.

5   In particular, the invention relates to an isolated polypeptide having the amino acid sequence X-Y-Z, wherein X is a polypeptide having the amino acid sequence, or portion thereof, consisting of the amino acid sequence of interferon beta; Y is an optional linker moiety; and Z is a polypeptide comprising at least a portion of a polypeptide other than interferon beta. Optional moiety Y and required moiety Z may be linked to either the N- or

10   C-terminus of inteferon beta (X). Preferably, X is human interferon-beta-1a. In the preferred embodiments, Z is at least a portion of a constant region of an immunoglobulin and can be derived from an immunoglobulin of the class selected from IgM, IgG, IgD, IgA, and IgE. If the class is IgG, then it is selected from one of IgG1, IgG2, IgG3 and IgG4. The constant region of human IgM and IgE contain 4 constant regions (CH1,

15   (hinge), CH2, CH3 and CH4, whereas the constant region of human IgG, IgA and IgD contain 3 constant regions (CH1, (hinge), CH2 and CH3. In the most preferred fusion proteins of the invention, the constant region contains at least the hinge, CH2 and CH3 domains. In other embodiments, moiety Z is at least a portion of a polypeptide that contains immunoglobulin-like domains. Examples of such other polypeptides include CD1,

20   CD2, CD4, and members of class I and class II major histocompatability antigens.

Another embodiment of the invention is a fusion protein having an amino terminal region consisting of the amino acid sequence of interferon beta or a portion thereof and having a carboxy terminal region comprising at least a portion of a protein other than interferon beta. The carboxy portion is preferably at least a portion of a constant region of

25   an immunoglobulin derived from an immunoglobulin of the class selected from IgM, IgG, IgD, IgA, and IgE. In the most preferred fusion proteins, the constant region contains at least the hinge, CH2 and CH3 domains.

Another embodiment of the invention is a fusion protein whose interferon beta moiety (e.g., X in the formula above) has been mutated to provide for muteins with

30   selectively enhanced antiviral and/or antiproliferative activity or other advantageous properties relative to non-mutated forms of interferon-beta-1a.

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Yet another embodiment of the invention is an isolated DNA encoding for the fusion proteins described above. The invention also pertains to a recombinant DNA comprising an isolated DNA encoding the fusion proteins described above and an expression control sequence, wherein the expression control sequence is operatively linked

5   to the DNA. The scope of the invention also includes host cells transformed with the recombinant DNA sequences of the invention.

The invention further pertains to a method of producing a recombinant polypeptide comprising: providing a population of host cells according to the invention; growing the population of cells under conditions whereby the polypeptide encoded by the recombinant

10   DNA is expressed; and isolating the expressed polypeptide.

A further aspect of the invention is a interferon-beta 1a fusion protein comprising interferon-beta-1a and additional polypeptide with which it is not natively associated, in substantially purified form, the fusion having an antiviral activity that is about equal to the anti-viral activity of interferon-beta-1a lacking the additional polypeptide.

15   Yet another aspect of the invention is a pharmaceutical composition comprising a therapeutically effective amount of an interferon-beta-1a fusion protein.

Yet another aspect of the invention is a method of inhibiting angiogenesis and neovascularization using the polypeptides of the invention.

BRIEF DESCRIPTION OF THE FIGURES

20   Figure 1 **cDNA and deduced amino acid sequence of a histidine tagged-interferon-beta fusion (also called "his IFN-beta" or "His$_6$ –tagged").** The full DNA and protein sequences of the his IFN-beta-1a are shown. The cleaved VCAM-1 signal sequence leaves 3 amino terminal residues (SerGlyGly) upstream of the histidine tag (His$_6$, positions 4-9). The enterokinase linker sequence (AspAspAspAspLys) is separate from the histidine tag

25   by a spacer (positions 10-12, SerSerGly). The natural IFN-beta-1a protein sequence spans positions (Met18-Asn183).

Figure 2.   **cDNA and deduced amino acid sequence for an interferon-beta-1a/Fc fusion.** The full DNA and protein sequences of the human IFN-beta-1a/mouse Fc are shown. The human IFN-beta-1a protein sequences span amino acid residues 1-166 (DNA

30   sequences 1-498). The enterokinase linker sequence spans amino acid residues 167-171

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(DNA sequences 499-513). The murine IgG2a heavy chain protein sequence spans
residues 172-399 (DNA sequences 514-437).

Figure 3.   **Binding of alanine substituted interferon-beta mutants to a dimeric**

5   **fusion protein comprised of the extracellular domain of the type I interferon receptor**

       chain, IFNAR2/Fc. The binding affinities of the alanine substituted IFN mutants (A1 - E)

       for the IFNAR2 receptor chain were determined as described in Example 1 (subsection D).

       The histogram presents their binding affinities in this assay relative to wild type his-IFN-

       beta (% w.t.). The % w. t. values were calculated as the (affinity of wild type his-IFN-

10   beta) / (affinity of mutant IFN-beta) x 100. The % w. t. (x) for multiple assays (n = 3) and

       an average % w.t. (x) for the experimental set are shown. Mutants A2, AB1, AB2, and E

       did not bind IFNAR2/Fc at concentrations 500-fold higher than the w.t. his-IFN-beta EC

       50 (*).

15   Figure 4.   **Binding of alanine substituted interferon-beta mutants to the type I**

       interferon cell surface receptor complexes ("IFNAR1/2 complex") expressed on

       Daudi Burkitt's lymphoma cells. The receptor binding properties of the alanine

       substitution mutants (A1 - E) were determined using a FACS based, cell surface receptor

       binding assay as described in Example 1 (subsection D). The histogram presents their

20   receptor binding affinities in this assay relative to wild type his-IFN-beta (% w.t.). The %

       w. t. for each mutant was calculated as (affinity of the w.t. his-IFN-beta)/(affinity of

       mutant IFN- beta) x 100. The % w.t. values ( ) from multiple assays under the histogram

       and an average of the % w.t. values for the experimental set (x) are shown.

25   Figure 5. **Antiviral activities of alanine substituted interferon-beta mutants**

       The antiviral activities of the alanine substitution mutants (A1- E) were determined

       on human A549 cells challenged with EMC virus as described in Example 1 (subsection

       E). The histogram presents their activities in this assay relative to wild type his-IFN-beta

       (% w.t.). The % w. t. was calculated as the inverse of the concentration of mutant IFN-

30   beta (50% cpe)/concentration of w.t. his-IFN-beta (50% cpe) x100. The % w.t ( ) for

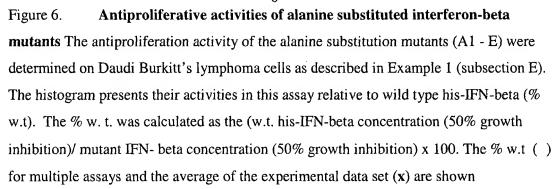   multiple assays and the average of the experimental data set (x) are shown.

Figure 6.   **Antiproliferative activities of alanine substituted interferon-beta**
mutants The antiproliferation activity of the alanine substitution mutants (A1 - E) were
determined on Daudi Burkitt's lymphoma cells as described in Example 1 (subsection E).
The histogram presents their activities in this assay relative to wild type his-IFN-beta (%
5   w.t). The % w. t. was calculated as the (w.t. his-IFN-beta concentration (50% growth
inhibition)/ mutant IFN- beta concentration (50% growth inhibition) x 100. The % w.t ( )
for multiple assays and the average of the experimental data set (x) are shown

Figure 7.   **Relative antiviral and antiproliferative activities of alanine substituted**
10   **interferon-beta mutants.** The relative activities of alanine substitution mutants (A1 - E)
in the antiviral (x axis) and antiproliferation (y axis) assays were compared. The average
percent wild type his-IFN-beta (% w. t.(x)) presented in Figures 5 and 6 were used for this
comparison. Those mutants with a coordinate loss/gain in activity would fall on or very
near the vertical line. Those mutants which have a disproportionate loss/gain in antiviral
15   or antiproliferation activities would fall significantly off the diagonal line (DE1, D, C1).
Significance was determined from consideration of standard deviations inherent in the
average % w. t. values used.

Figure 8.   **Antiviral Activity of interferon-beta-1a/Ig fusion.**
20   The activity of interferon-beta-1a (used as AVONEX ®) or interferon-beta-
1a/murine Ig2a fusion at the concentrations indicated on the X axis were assessed in
antiviral assays using human lung carcinoma (A549) cells challenged with EMC virus.
Following a two day incubation with virus, viable cells were stained with MTT, the plates
were read at 450 nm, and the absorbance which is reflective of cell viability is shown on
25   the Y axis. The standard deviations are shown as error bars. The concentration of
interferon-beta-1a (used as AVONEX ® bulk intermediate) which offered (50%
maximum OD450) and therefore 50% viral killing (the "50% cytopathic effect") was about
0.4 pM and the 50% cytopathic effect for interferon-beta-1a fusion was about 0.15 pM.

30   Figure 9.   **Measurements of interferon-beta antiviral activity in the plasma of**
mice treated with interferon-beta-1a/Fc fusion or interferon-beta-1a.

Mice are injected iv with either 50,000 Units of interferon-beta-1a (used as

AVONEX® bulk intermediate) or 50,000 Units of interferon-beta-1a/Fc fusion. Blood

from these mice is obtained via retro-orbital bleeds at various times after interferon

injection as indicated on the X axis. There are at least 3 mice bled at each time point, and

5   plasma is prepared and frozen until the time interferon-beta activity is evaluated in

antiviral assays using human lung carcinoma (A549) cells challenged with

encephalomyocarditis virus. Viable cells were stained with a solution of MTT, the plates

were read at 450 nm, to determine the absorbance which is reflective of cell viability and

interferon-beta activity. Standard curves were generated for each plate using interferon-

10   beta-1a as AVONEX ® and used to determine the amount of interferon-beta activity in

each sample. Data from the individual animals are shown.

Figure 10.   Full DNA and protein sequences of the open reading frames of a direct

fusion of human IFN beta and human IgG1Fc (ZL5107)

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Figure 11.   Full DNA and protein sequences of the open reading frame of a fusion

protein consisting of human IFN beta/G4S linker/human IgG1FC (ZL6206).

Figure 12.   Schematic representation of overall cloning and expression strategy.

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DETAILED DESCRIPTION

All references cited in the Detailed Description are incorporated herein by references,

unless stipulated otherwise. The following terms are used herein:

I. Definitions:

25   Interferon- An "interferon" (also referred to as "IFN") is a small, species-specific,

single chain polypeptide, produced by mammalian cells in response to exposure to a

variety of inducers such as viruses, polypeptides, mitogens and the like. The most

preferred interferon used in the invention is glycosylated, human, interferon-beta that is

glycosylated at residue 80 (Asn 80) and that is preferably derived via recombinant DNA

30   technologies. This preferred glycosylated interferon beta is called "interferon-beta-1a" (or

"IFN-beta-1a" or "IFN-ꓱ-1a" or or "interferon beta 1a" or "interferon-beta-1a" or

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"interferon-ꓱ-1a", all used interchangeably). The term "interferon-beta-1a" is also intended to encompass all mutant forms (i.e., Example 1) provided that the mutants are also glycosylated at the Asn 80 residue.

Recombinant DNA methods for producing proteins, including interferons are known. See for example, U.S. Patents **4,399,216, 5,149,636, 5,179,017** (Axel et al) and **4,470,461** (Kaufman).

Preferred interferon-beta-1a polynucleotides that may be used in the present methods of the invention are derived from the wild-type interferon beta gene sequences of various vertebrates, preferably mammals and are obtained using methods that are well-known to those having ordinary skill in the art such as the methods described in the following U.S. Patents: **U. S Patent 5,641,656** (issued Jun. 24, 1997: DNA encoding avian type I interferon proprotein and mature avian type I interferon), **U.S. Patent 5,605,688** (Feb. 25, 1997- recombinant dog and horse type I interferons); **U.S. Patent 5,231,176** (Jul. 27, 1993, DNA molecule encoding a human leukocyte interferon);); **U.S. Patent 5,071,761** (Dec. 10, 1991, DNA sequence coding for sub-sequences of human lymphoblastoid interferons LyIFN- alpha -2 and LyIFN- alpha -3); **U.S. Patent 4,970,161** (Nov. 13, 1990, DNA sequence coding for human interferon- gamma)**; U.S. Patent 4,738,931** (Apr. 19, 1988, DNA containing a human interferon beta gene); **U.S. Patent 4,695,543** (Sep. 22, 1987, human alpha-interferon Gx-1 gene and U.S. Patent **4,456,748** (Jun. 26, 1984, DNA encoding sub-sequences of different, naturally, occurring leukocyte interferons).

Mutants of interferon-beta-1a may be used in accordance with this invention. Mutations are developed using conventional methods of directed mutagenesis, known to those of ordinary skill in the art. Moreover, the invention provides for functionally equivalent interferon-beta-1a polynucleotides that encode for functionally equivalent interferon-beta-1a polypeptides.

A first polynucleotide encoding interferon-beta-1a is "functionally equivalent" compared with a second polynucleotide encoding interferon-beta-1a if it satisfies at least one of the following conditions:

(a): the "functional equivalent" is a first polynucleotide that hybridizes to the second polynucleotide under standard hybridization conditions and/or is degenerate to the

first polynucleotide sequence. Most preferably, it encodes a mutant interferon having the [therapeutic] activity of an interferon-beta-1a;

(b) the "functional equivalent" is a first polynucleotide that codes on expression for an amino acid sequence encoded by the second polynucleotide.

5   In summary, the term "interferon" includes, but is not limited to, the agents listed above as well as their functional equivalents. As used herein, the term "functional equivalent" therefore refers to an interferon-beta-1a protein or a polynucleotide encoding the interferon-beta-1a protein that has the same or an improved beneficial effect on the mammalian recipient as the interferon of which it is deemed a functional equivalent. As

10   will be appreciated by one of ordinary skill in the art, a functionally equivalent protein can be produced by recombinant techniques, e.g., by expressing a "functionally equivalent DNA". Accordingly, the instant invention embraces interferon-beta-1a proteins encoded by naturally-occurring DNAs, as well as by non-naturally-occurring DNAs which encode the same protein as encoded by the naturally-occurring DNA. Due to the degeneracy of the

15   nucleotide coding sequences, other polynucleotides may be used to encode interferon-beta-1a. These include all, or portions of the above sequences which are altered by the substitution of different codons that encode the same amino acid residue within the sequence, thus producing a silent change. Such altered sequences are regarded as equivalents of these sequences. For example, Phe (F) is coded for by two codons, TTC or

20   TTT, Tyr (Y) is coded for by TAC or TAT and His (H) is coded for by CAC or CAT. On the other hand, Trp (W) is coded for by a single codon, TGG. Accordingly, it will be appreciated that for a given DNA sequence encoding a particular interferon there will be many DNA degenerate sequences that will code for it. These degenerate DNA sequences are considered within the scope of this invention.

25   "fusion"- refers to a co-linear, covalent linkage of two or more proteins or fragments thereof via their individual peptide backbones, most preferably through genetic expression of a polynucleotide molecule encoding those proteins. It is preferred that the proteins or fragments thereof are from different sources. Thus, preferred fusion proteins include an interferon-beta-1a protein or fragment covalently linked to a second moiety that

30   is not an interferon. Specifically, an "interferon-beta/Ig fusion" is a protein comprising an interferon beta molecule of the invention (i.e., interferon-beta-1a), or fragment thereof

whose N-terminus or C-terminus is linked to an N-terminus of an immunoglobulin chain wherein a portion of the N-terminus of the immunoglobulin is replaced with the interferon beta. A species of interferon-beta/Ig fusion is an "interferon-beta/Fc fusion" which is a protein comprising an interferon beta molecule of the invention (i.e., interferon-beta-1a)

5   linked to at least a part of the constant domain of an immunoglobulin. A preferred Fc fusion comprises an interferon beta molecule of the invention linked to a fragment of an antibody containing the C terminal domain of the heavy immunoglobulin chains.

Also, the term "fusion protein" means an interferon beta protein chemically linked via a mono- or hetero- functional molecule to a second moiety that is not an interferon beta

10   protein and is made de novo from purified protein as described below.

"Recombinant," as used herein, means that a protein is derived from recombinant, mammalian expression systems. Protein expressed in most bacterial cultures, e.g., E. coli, will be free of glycan so these expression systems are not preferred. Protein expressed in yeast may have oligosaccharide structures that are different from that

15   expressed in mammalian cells.

"Biologically active," as used throughout the specification as a characteristic of interferon-beta 1a, means that a particular molecule shares sufficient amino acid sequence homology with the embodiments of the present invention disclosed herein to be capable of antiviral activity as measured in an in vitro antiviral assay of the type

20   shown in Example 1, as described below.

A "therapeutic composition" as used herein is defined as comprising the proteins of the invention and other physiologically compatible ingredients. The therapeutic composition may contain excipients such as water, minerals and carriers such as protein.

25   "amino acid"- a monomeric unit of a peptide, polypeptide, or protein. There are twenty amino acids found in naturally occurring peptides, polypeptides and proteins, all of which are L-isomers. The term also includes analogs of the amino acids and D-isomers of the protein amino acids and their analogs.

A "derivatized" amino acid is a natural or nonnatural amino acid in which the

30   normally occurring side chain or end group (or sugar moiety in the case of interferon-beta-1a) is modified by chemical reaction. Such modifications include, for example,

gamma-carboxylation, beta-carboxylation, pegylation, sulfation, sulfonation, phosphorylation, amidization, esterification, N-acetylation, carbobenzylation, tosylation, and other modifications known in the art. A "derivatized polypeptide" is a polypeptide containing one or more derivatized amino acids and/or one or more

5   derivatized sugars, if the polypeptide is glycosylated.

"protein"- any polymer consisting essentially of any of the 20 amino acids. Although "polypeptide" is often used in reference to relatively large polypeptides, and "peptide" is often used in reference to small polypeptides, usage of these terms in the art overlaps and is varied. The term "protein" as used herein refers to peptides, proteins

10   and polypeptides, unless otherwise noted.

"functional equivalent" of an amino acid residue is an amino acid having similar physico-chemical properties as the amino acid residue that was replaced by the functional equivalent.

"mutant" - any change in the genetic material of an organism, in particular

15   any change (i.e., deletion, substitution, addition, or alteration) in a wild-type polynucleotide sequence or any change in a wild-type protein. The term "mutein" is used interchangeably with "mutant".

"wild-type" - the naturally-occurring polynucleotide sequence of an exon of a protein, or a portion thereof, or protein sequence, or portion thereof, respectively, as it

20   normally exists *in vivo*.

"standard hybridization conditions"- salt and temperature conditions substantially equivalent to 0.5 X SSC to about 5 X SSC and 65 ° C for both hybridization and wash. The term "standard hybridization conditions" as used herein is therefore an operational definition and encompasses a range of hybridization conditions.

25   Higher stringency conditions may, for example, include hybridizing with plaque screen buffer (0.2% polyvinylpyrrolidone, 0.2% Ficoll 400; 0.2% bovine serum albumin, 50 mM Tris-HCl (pH 7.5); 1 M NaCl; 0.1% sodium pyrophosphate; 1 % SDS); 10% dextran sulfate, and 100 μg/ml denatured, sonicated salmon sperm DNA at 65 ° C for 12-20 hours, and washing with 75 mM NaCl/7.5 mM sodium citrate (0.5 x SSC)/1%

30   SDS at 65° C. Lower stringency conditions may, for example, include hybridizing with plaque screen buffer, 10% dextran sulfate and 110 μg/ml denatured, sonicated salmon

sperm DNA at 55 ° C for 12-20 hours, and washing with 300 mM NaCl/30mM sodium

citrate (2.0 X SSC)/1% SDS at 55 ° C. See also **Current Protocols in Molecular**

Biology, John Wiley & Sons, Inc. New York, Sections 6.3.1-6.3.6, (1989).

"expression control sequence"- a sequence of polynucleotides that controls

5   and regulates expression of genes when operatively linked to those genes.

"operatively linked"- a polynucleotide sequence (DNA, RNA) is operatively

linked to an expression control sequence when the expression control sequence controls

and regulates the transcription and translation of that polynucleotide sequence. The

term "operatively linked" includes having an appropriate start signal (e.g., ATG) in

10   front of the polynucleotide sequence to be expressed and maintaining the correct

reading frame to permit expression of the polynucleotide sequence under the control of

the expression control sequence and production of the desired polypeptide encoded by

the polynucleotide sequence.

"expression vector"- a polynucleotide, such as a DNA plasmid or phage

15   (among other common examples) which allows expression of at least one gene when

the expression vector is introduced into a host cell. The vector may, or may not, be able

to replicate in a cell.

"Isolated" (used interchangeably with "substantially pure")- when applied to

nucleic acid i.e., polynucleotide sequences, that encode polypeptides, means an RNA or

20   DNA polynucleotide, portion of genomic polynucleotide, cDNA or synthetic

polynucleotide which, by virtue of its origin or manipulation: (i) is not associated with

all of a polynucleotide with which it is associated in nature (e.g., is present in a host cell

as an expression vector, or a portion thereof); or (ii) is linked to a nucleic acid or other

chemical moiety other than that to which it is linked in nature; or (iii) does not occur in

25   nature. By "isolated" it is further meant a polynucleotide sequence that is: (i) amplified

in vitro by, for example, polymerase chain reaction (PCR); (ii) chemically synthesized;

(iii) recombinantly produced by cloning; or (iv) purified, as by cleavage and gel

separation.

Thus, "substantially pure nucleic acid" is a nucleic acid which is not

30   immediately contiguous with one or both of the coding sequences with which it is

normally contiguous in the naturally occurring genome of the organism from which the

nucleic acid is derived. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional sequences.

"Isolated" (used interchangeably with "substantially pure")- when applied to polypeptides means a polypeptide or a portion thereof which, by virtue of its origin or manipulation: (i) is present in a host cell as the expression product of a portion of an expression vector; or (ii) is linked to a protein or other chemical moiety other than that to which it is linked in nature; or (iii) does not occur in nature. By "isolated" it is further meant a protein that is: (i) chemically synthesized; or (ii) expressed in a host cell and purified away from associated proteins. The term generally means a polypeptide that has been separated from other proteins and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances such as antibodies or gel matrices (polyacrylamide) which are used to purify it.

"heterologous promoter"- as used herein is a promoter which is not naturally associated with a gene or a purified nucleic acid.

"Homologous"- as used herein is synonymous with the term "identity" and refers to the sequence similarity between two polypeptides, molecules or between two nucleic acids. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit (for instance, if a position in each of the two DNA molecules is occupied by adenine, or a position in each of two polypeptides is occupied by a lysine), then the respective molecules are homologous at that position. The percentage homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For instance, if 6 of 10 of the positions in two sequences are matched or are homologous, then the two sequences are 60% homologous. By way of example, the DNA sequences CTGACT and CAGGTT share 50% homology (3 of the 6 total positions are matched). Generally, a comparison is made when two sequences are aligned to give maximum homology. Such alignment can be provided using, for instance, the method of Needleman et al., *J. Mol Biol.* 48: 443-453 (1970), implemented conveniently by computer programs such as the Align program (DNAstar, Inc.). Homologous sequences share identical or similar amino acid residues, where similar residues are conservative substitutions for, or "allowed point mutations" of, corresponding amino acid residues in an

aligned reference sequence. In this regard, a "conservative substitution" of a residue in a reference sequence are those substitutions that are physically or functionally similar to the corresponding reference residues, e.g., that have a similar size, shape, electric charge, chemical properties, including the ability to form covalent or hydrogen bonds, or the like.

5   Particularly preferred conservative substitutions are those fulfilling the criteria defined for an "accepted point mutation" in Dayhoff et al., 5: **Atlas of Protein Sequence and Structure,** 5: Suppl. 3, chapter 22: 354-352, Nat. Biomed. Res. Foundation, Washington, D.C. (1978).

The terms "polynucleotide sequence" and "nucleotide sequence" are also used
10   interchangeably herein.

The terms "neovascularization" and "angiogenesis" mean, in their broadest sense, the recruitment of new blood vessels. In particular, "angiogenesis" also refers to the recruitment of new blood vessels at a tumor site.

"IFNAR2", "IFNAR1", "IFNAR1/2" refer to the proteins knows to compose the
15   cell surface type I interferon receptor. The extracellular portion (ectodomain) portion of the IFNAR2 chain alone can bind interferon alpha or beta.

Practice of the present invention will employ, unless indicated otherwise, conventional techniques of cell biology, cell culture, molecular biology, microbiology, recombinant DNA, protein chemistry, and immunology, which are within the skill of
20   the art. Such techniques are described in the literature. See, for example, **Molecular Cloning: A Laboratory Manual,** 2nd edition. (Sambrook, Fritsch and Maniatis, eds.), Cold Spring Harbor Laboratory Press, 1989; **DNA Cloning**, Volumes I and II (D.N. Glover, ed), 1985; **Oligonucleotide Synthesis**, (M.J. Gait, ed.), 1984; U.S. Patent No. 4,683,195 (Mullis et al.,); **Nucleic Acid Hybridization** (B.D. Hames and S.J. Higgins,
25   eds.), 1984; Transcription and Translation (B.D. Hames and S.J. Higgins, eds.), 1984; **Culture of Animal Cells** (R.I. Freshney, ed). Alan R. Liss, Inc., 1987; **Immobilized Cells and Enzymes,** IRL Press, 1986; **A Practical Guide to Molecular Cloning** (B. Perbal), 1984; **Methods in Enzymology,** Volumes 154 and 155 (Wu et al., eds), Academic Press, New York; **Gene Transfer Vectors for Mammalian Cells** (J.H.
30   Miller and M.P. Calos, eds.), 1987, Cold Spring Harbor Laboratory; **Immunochemical Methods in Cell and Molecular Biology** (Mayer and Walker, eds.), Academic Press,

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London, 1987; **Handbook of Experiment Immunology,** Volumes I-IV (D.M. Weir and C.C. Blackwell, eds.), 1986; **Manipulating the Mouse Embryo,** Cold Spring Harbor Laboratory Press, 1986.

II. Production and Expression of Fusion Proteins

5   The present invention relates to a system for the generation of interferon-beta-1a fusion proteins. In particular, the present invention relates to these proteins as well as the recombinant DNA molecules utilized in their production.

The production of the polypeptides of this invention may be achieved by a variety of methods known in the art. For example, full length interferon-beta-1a or truncated

10   forms of interferon-beta-1a may be produced by known recombinant DNA techniques using cDNAs (see below).

A gene which encodes the desired interferon-beta-1a polypeptide may be designed based on the amino acid sequence of the desired polypeptide. Standard methods may then be applied to synthesize the gene. For example, the amino acid sequence may be used to

15   construct a back-translated gene. A DNA oligomer containing a nucleotide sequence capable of coding for interferon-beta-1a may be made in a single step. Alternately, several smaller oligonucleotides coding for portions of the desired interferon-beta-1a may be synthesized and then ligated together. Preferably, the DNA sequence encoding the interferon-beta-1a moiety will be made as several separate oligonucleotides which are

20   subsequently linked together. (See Example 2). The individual oligonucleotides typically contain 5' or 3' overhangs for complementarity assembly.

Once assembled, preferred genes will be characterized by sequences that are recognized by restriction endonucleases (including unique restriction sites for direct assembly into a cloning or expression vector), preferred codons taking into consideration

25   the host expression system to be used (preferably a mammalian cell), and a sequence which, when transcribed, produces a stable, efficiently translated RNA. Proper assembly may be confirmed by nucleotide sequencing, restriction mapping, and expression of a biologically active polypeptide in a suitable host.

Mammalian interferon beta cDNAs may be isolated by using an appropriate human

30   interferon beta DNA sequence as a probe for screening a particular mammalian cDNA library by cross-species hybridization. Mammalian interferon beta used in the present

invention includes, by way of example, primate, human, murine, canine, feline, bovine, equine and porcine interferon beta. Mammalian interferon beta can be obtained by cross species hybridization, using a single stranded cDNA derived from the human interferon beta DNA sequence as a hybridization probe to isolate interferon beta cDNAs from

5   mammalian cDNA libraries. Among the methods that can be used for isolating and cloning interferon gene sequences are those methods found in the U.S. Patents summarized above. Of particular relevance, however, are the teachings of **U.S. Patent 4,738,931** (Apr. 19, 1988) describing DNA containing a human interferon beta gene.

The present invention also related to recombinant DNA molecules comprising the

10   aforementioned DNA sequences. The recombinant DNA molecules of this invention are capable of directing expression of the polypeptides of the invention in hosts transformed therewith. A DNA sequence encoding a fusion polypeptide of the invention must be operatively linked to an expression control sequence for such expression. To provide for adequate transcription of the recombinant constructs of the invention, a suitable

15   promoter/enhancer sequence may preferably be incorporated into the recombinant vector, provided that the promoter/expression control sequence is capable of driving transcription of a nucleotide sequence encoding a glycosylated interferon beta. Promoters which may be used to control the expression of the immunoglobulin-based fusion protein include, but are not limited to, the SV40 early promoter region (Benoist and Chambon, 1981, Nature

20   290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:144-1445), the regulatory sequences of the metallothionine gene (Brinster et al., 1982, Nature 296:39-42); plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella et al., Nature

25   303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, et al., 1981, Nucl. Acids Res. 9:2871), and the promoter for the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al., 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phophatase

30   promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region

which is active in pancreatic cells (Swift et al., 1984, Cell 38:639-646; Ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene enhancers or promoters which are active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122); immunoglobulin gene enhancers or promoters

5   which are active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-1444); the cytomegalovirus early promoter and enhancer regions (Boshart et al., 1985, Cell 41:521-530); mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495); albumin gene control region

10   which is active in liver (Pinkert et al., 1987, Genes and Devel. 1:268-276); alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58); alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al, 1987, Genes and Devel. 1:161-171); beta-globin gene control region which is active in myeloid cells (Mogram et al.,

15   1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286); and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-

20   1378). Prokaryotic expression systems such as the LAC, or beta -lactamase promoter (Villa-Kamaroff, et al., 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731) are not presently preferred inasmuch as the expressed interferon beta will not be glycosylated. Nevertheless, prokaryotic expression systems that will allow glycosylation of interferon beta in either prokaryotic or eukaryotic hosts are encompassed within the scope of the

25   invention.

The expression vectors which can be used include, but are not limited to, the following vectors or their derivatives: human or animal viruses such as vaccinia virus, adenovirus or retroviral based vectors; insect viruses such as baculovirus; yeast vectors; bacteriophage vectors (e.g., lambda), and plasmid and cosmid DNA vectors, to name but a

30   few. Specifically, useful expression vectors for the preferred eukaryotic hosts include vectors comprising expression control sequences from SV40, bovine papillomavirus,

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cytomegalovirus. Further, within each specific expression vector, various sites may be selected for insertion of these DNA sequences. These sites are usually designated by the restriction endonuclease which cuts them. They are well-recognized by those of skill in the art. It will be appreciated that a given expression vector useful in this invention need

5 not have a restriction endonuclease site for insertion of the chosen DNA fragment. Instead, the vector may be joined by the fragment by alternate means.

The expression vector, and the site chosen for insertion of a selected DNA fragment and operative linking to an expression control sequence, is determined by a variety of factors such as: the number of sites susceptible to a particular restriction enzyme, the size

10 of the polypeptide, how easily the polypeptide is proteolytically degraded, and the like. The choice of a vector and insertion site for a given DNA is determined by a balance of these factors.

The recombinant constructs of the invention may be introduced into host cells which are capable of expressing the fusion protein using any method known in the art,

15 including transformation (for example, using DEAE-dextran or calcium phosphate techniques), transfection, microinjection, infection, cell gun, and electroporation. Any host cell type may be utilized provided that the fusion protein recombinant nucleic acid sequences would be adequately transcribed into mRNA in that cell type and the cell can glycosylate the protein. In addition, the recombinant nucleic acid constructs of the

20 invention may be used to create non-human transgenic animals capable of producing the immunoglobulin based fusion protein. In preferred embodiments of the invention, the host cell is a mammalian cell, such as a COS or CHO cell.

Successful incorporation of these polynucleotide constructs into a given expression vector may be identified by three general approaches: (a) DNA-DNA hybridization, (b)

25 presence or absence of "marker" gene functions, and (c) expression of inserted sequences. In the first approach, the presence of the interferon-beta-1a gene inserted in an expression vector can be detected by DNA-DNA hybridization using probes comprising sequences that are homologous to the inserted fusion protein gene. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or

30 absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics such as G418, transformation phenotype, occlusion body formation in

baculovirus, etc.) caused by the insertion of foreign genes in the vector. For example, if the polynucleotide is inserted so as to interrupt a marker gene sequence of the vector, recombinants containing the insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by

5   assaying the foreign gene product expressed by the recombinant vector. Such assays can be based, for example, on the physical or functional properties of the gene product in bioassay systems.

It will be appreciated that not all host/expression vector combinations will function with equal efficiency in expressing DNA sequences encoding the polypeptides of this

10   invention. However, a particular selection of a host-expression vector combination may be made by those of skill in the art after due consideration of the principles set forth herein without departing from the scope of the invention.

The preferred embodiment of the invention contemplates fusion proteins and DNA sequences coding for them. These fusion proteins have an amino-terminal region

15   characterized by the amino acid sequence of interferon-beta-1a and a carboxy-terminal region comprising a domain of a protein other than interferon-beta-1a. A preferred generic formula for such a protein is a protein having a primary amino acid sequence X-Y-Z, wherein X is a polypeptide having the amino acid sequence, or portion thereof, consisting of the amino acid sequence of human interferon beta; Y is an optional linker moiety; and Z

20   is a polypeptide comprising at least a portion of a polypeptide other than human interferon beta. In one embodiment, moiety Z can be a portion of a polypeptide that contains immunoglobulin-like domains. Examples of such other polypeptides include CD1, CD2, CD4, and members of class I and class II major histocompatability antigens. See U.S. 5,565,335 (Capon et al.) for examples of such polypeptides.

25   Moiety Z can include, for instance, a plurality of histidine residues or, preferably, the Fc region of an immunoglobulin, "Fc" defined herein as a fragment of an antibody containing the C terminal domain of the heavy immunoglobulin chains.

In the most preferred fusion proteins, the interferon-beta-1a polypeptide is fused via its C-terminus to at least a portion of the Fc region of an immunoglobulin. The

30   interferon-beta-1a forms the amino-terminal portion, and the Fc region forms the carboxy terminal portion. In these fusion proteins, the Fc region is preferably limited to the

constant domain hinge region and the CH2 and CH3 domains. The Fc region in these

fusions can also be limited to a portion of the hinge region, the portion being capable of

forming intermolecular disulfide bridges, and the CH2 and CH3 domains, or functional

equivalents thereof. These constant regions may be derived from any mammalian source

5   (preferably human) and may be derived from any appropriate class and/or isotype,

including IgA, IgD, IgM, IgE and IgG1, IgG2, IgG3 and IgG4.

Recombinant nucleic acid molecules which encode the Ig fusions may be obtained

by any method known in the art (Maniatis et al., 1982, Molecular Cloning; A Laboratory

Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) or obtained from

10   publicly available clones. Methods for the preparation of genes which encode the heavy or

light chain constant regions of immunoglobulins are taught, for example, by Robinson, R.

et al., PCT Application, Publication No. WO87-02671. The cDNA sequence encoding the

interferon molecule or fragment may be directly joined to the cDNA encoding the heavy Ig

contant regions or may be joined via a linker sequence. In further embodiments of the

15   invention, a recombinant vector system may be created to accommodate sequences

encoding interferon beta in the correct reading frame with a synthetic hinge region.

Additionally, it may be desirable to include, as part of the recombinant vector system,

nucleic acids corresponding to the 3' flanking region of an immunoglobulin gene including

RNA cleavage/polyadenylation sites and downstream sequences. Furthermore, it may be

20   desirable to engineer a signal sequence upstream of the immunoglobulin fusion protein-

encoding sequences to facilitate the secretion of the fused molecule from a cell

transformed with the recombinant vector.

The present invention provides for dimeric fusion molecules as well

as monomeric or multimeric molecules comprising fusion proteins. Such multimers may

25   be generated by using those Fc regions, or portions thereof, of Ig molecules which are

usually multivalent such as IgM pentamers or IgA dimers. It is understood that a J chain

polypeptide may be needed to form and stabilize IgM pentamers and IgA dimers.

Alternatively, multimers of interferon-beta-1a fusion proteins may be formed using a

protein with an affinity for the Fc region of Ig molecules, such as Protein A. For instance,

30   a plurality of interferon-beta-1a/ immunoglobulin fusion proteins may be bound to Protein

A-agarose beads.

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These polyvalent forms are useful since they possess multiple interferon beta receptor binding sites. For example, a bivalent soluble interferon-beta-1a may consist of two tandem repeats of amino acids 1 to 166 of SEQ ID NO: 2 (or those encoded by nucleic acids numbered 1 to 498 of SEQ. ID.NO:1) (moiety X in the generic formula) separated by a linker region (moiety Y), the repeats bound to at least a portion of an immunoglobulin constant domain (moiety Z). Alternate polyvalent forms may also be constructed, for example, by chemically coupling interferon-beta-1a/Ig fusions to any clinically acceptable carrier molecule, a polymer selected from the group consisting of Ficoll, polyethylene glycol or dextran using conventional coupling techniques. Alternatively, interferon-beta-1a may be chemically coupled to biotin, and the biotin-interferon beta Fc conjugate then allowed to bind to avidin, resulting in tetravalent avidin/biotin/interferon beta molecules. Interferon-beta-1a/Ig fusions may also be covalently coupled to dinitrophenol (DNP) or trinitrophenol (TNP) and the resulting conjugate precipitated with anti-DNP or anti-TNP-IgM, to form decameric conjugates with a valency of 10 for interferon beta receptor binding sites

The interferon-beta-1a proteins, fragments, and fusion proteins of the invention may be isolated and purified in accordance with conventional conditions, such as extraction, precipitation, chromatography, affinity chromatography, electrophoresis or the like. For example, the interferon proteins and fragments may be purified by passing a solution thereof through a column having an interferon receptor immobilized thereon (see U.S. Pat. No. 4,725,669). The bound interferon molecule may then be eluted by treatment with a chaotropic salt or by elution with aqueous acetic acid. The immunoglobulin fusion proteins may be purified by passing a solution containing the fusion protein through a column which contains immobilized protein A or protein G which selectively binds the Fc portion of the fusion protein. See, for example, Reis, K. J., et al., J. Immunol. 132:3098-3102 (1984); PCT Application, Publication No. WO87/00329. The chimeric antibody may then be eluted by treatment with a chaotropic salt or by elution with aqueous acetic acid.

Alternatively the interferon proteins and immunoglobulin-fusion molecules may be purified on anti-interferon antibody columns, or on anti-immunoglobulin antibody columns to give a substantially pure protein. By the term "substantially pure" is intended that the

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protein is free of the impurities that are naturally associated therewith. Substantial purity may be evidenced by a single band by electrophoresis.

An example of a useful interferon-beta-1a/Ig fusion protein of this invention is that of SEQ ID NO: 2, which is secreted into the cell culture by eukaryotic cells containing the
5   expression plasmid pCMG261 (See Example 2). This protein consists of the mature human interferon-beta-1a fused to a portion of the hinge region and the CH2 and CH3 constant domains of murine Ig. This contains a sufficient portion of the murine immunoglobulin to be recognized by the Fc binding protein, Protein A.

Other fusion proteins of the invention incorporating human interferon-beta-1a are
10   shown: (a) in SEQ ID NOS: 3 and 4 for the cDNA and deduced amino acids sequences, respectively of a his tagged-interferon-beta-1a fusion (also shown in Figure 1) and; (b) in SEQ NO: 1 for the cDNA encoding the interferon-beta-1a/ Ig fusion protein of SEQ ID NO: 2 (also shown in Figure 2).

The preferred interferon-beta-1a proteins of the invention include the novel
15   "junction" DNA sequence SEQ ID NO: 5 and amino acid SEQ ID NO: 6. SEQ ID NO: 5 represents the 11 triplet codons on either side of the junction between human interferon beta DNA and the DNA encoding a human immunoglobulin constant region (see Example 5: SEQ ID NOS: 41 and 42). Specifically, in SEQ ID NO: 5, the DNA encoding human interferon-beta-1a ends at nucleotide triplet 568-570 (AAC) and DNA encoding a human
20   IgG1 constant region starts at the triplet (GAC) beginning with nucleotide number 574 of SEQ ID NO: 41. The corresponding deduced amino acid "junction" sequence is represented in SEQ ID NO: 6 and is based on SEQ ID NO: 42. Another unique "junction" sequence is defined that includes a linker sequence in the final DNA construct (See Example 5: SEQ ID NOS: 43 and 44). This "junction" DNA and amino acid sequence are
25   represented in SEQ ID NO: 7 and 8, respectively, which shows the 11 triplet codons on either side of the junction directly between the end of the interferon-beta-1a sequence (nucleotide number 570 in SEQ ID NO: 43) and the linker sequence (nucleotides 571 to 585 in SEQ ID NO:43; GGGGS in SEQ ID NO: 8).

The DNA "junction" sequences can be used as DNA probes and may be the
30   minimum DNA needed for hybridization under standard conditions to any DNA sequence encoding any interferon-beta-1a/Ig fusion protein. Nevertheless, provided that the whole

probe hybridizes to both sides of the junction and both sides of the interferon beta /constant

region junction participate in the hybridization, smaller sequences may exist. Furthermore,

persons having ordinary skill in the art will understand that DNA sequences larger than

SEQ ID NO:5 or 7 will be suitable for hybridization as well. One of ordinary skill in the

5   art can test if a particular probe such as SEQ ID NO: 5 or 7 are capable of hybridizing on

both sides of the junction by labelling the 5' end of either a single strand sense

oligonucleotide or a single strand anti-sense oligonucleotide with an appropriately labelled

phosphate of ATP using polynucleotide kinase. A sequence of the invention must

hybridize to, and thus be labelled by both oligonucleotide probes. It is further understood

10   that the invention encompasses fully degenerate sequences encoding the junction SEQ ID

NO: 5 or 7.

III. Other Variants of Interferon Fusion Polypeptides

        Derivatives of proteins of the invention also include various structural forms of

the primary protein which retain biological activity. Due to the presence of ionizable

15   amino and carboxyl groups, for example, interferon beta fusion protein may be in the

form of acidic or basic salts, or may be in neutral form. Individual amino acid residues

may also be modified by oxidation or reduction. Further, the primary amino acid

structure (including the N- and/or C-terminal ends) or the glycan of the interferon-beta-1a

may be modified ("derivatized") by forming covalent or aggregative conjugates with

20   other chemical moieties, such as glycosyl groups, polyalkylene glycol polymers such as

polyethylene glycol (PEG: see co-pending and commonly assigned application Serial

Number 60/104,491 and 60/720,237), lipids, phosphate, acetyl groups and the like, or by

creating amino acid sequence mutants.

        Other derivatives of interferon beta/ Ig include covalent or aggregative conjugates

25   of interferon beta or its fragments with other proteins or polypeptides, such as by

synthesis in recombinant culture as additional N-termini, or C-termini. For example, the

conjugated peptide may be a signal (or leader) polypeptide sequence at the N-terminal

region of the protein which co-translationally or post-translationally directs transfer of the

protein from its site of synthesis to its site of function inside or outside of the cell

30   membrane or wall (e.g., the yeast *alpha* -factor leader). Interferon beta receptor proteins

can comprise peptides added to facilitate purification or identification of interferon beta

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(e.g., histdine/interferon-beta-1a fusions). The amino acid sequence of interferon beta can also be linked to the peptide Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys (DYKDDDDK) (Hopp et al., Bio/Technology 6:1204,1988.) The latter sequence is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid

5 assay and facile purification of expressed recombinant protein. This sequence is also specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing.

Other analogs include interferon beta fusion Fc protein or its biologically active fragments whose interferon beta sequences differ from those shown in SEQ ID NOS: 2,

10 4,6 or 8 by one or more conservative amino acid substitutions or by one or more non conservative amino acid substitutions, or by deletions or insertions which do not abolish the isolated protein's biological activity. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics such as substitutions within the following groups: valine, alanine and glycine; leucine and

15 isoleucine; aspartic acid and glutamic acid; asparagine and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine. The non-polar hydrophobic amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine and glutamine. The positively

20 charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Other conservative substitutions can be readily known by workers of ordinary skill. For example, for the amino acid alanine, a conservative substitution can be taken from any one of D-alanine, glycine, beta-alanine, L-cysteine and D-cysteine. For lysine, a replacement can be any

25 one of D-lysine, arginine, D-arginine, homo-arginine, methionine, D-methionine, ornithine, or D-ornithine. Generally, substitutions that may be expected to induce changes in the functional properties of isolated polypeptides are those in which: (i) a polar residue, e.g., serine or threonine, is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, or alanine; (ii) a cysteine residue is substituted for (or

30 by) any other residue; (iii) a residue having an electropositive side chain, e.g., lysine, arginine or histidine, is substituted for (or by) a residue having an electronegative side

chain, e.g., glutamic acid or aspartic acid; or (iv) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having such a side chain, e.g., glycine. Included in the invention are isolated molecules that are: allelic variants, natural mutants, induced mutants, proteins encoded by DNA that hybridize under high or low stringency

5   conditions to a nucleic acid which encodes a polypeptide such as SEQ. ID. NOS.2, 4, 6 or 8.

We developed interferon-beta-1a mutants that are further variants of the interferon-beta-1a moiety of the invention. These interferon-beta-1a moieties may be particularly useful inasmuch as they display novel properties not found in the wild type interferon-beta-

10   1a (See Example 1). Briefly, we undertook a mutational analysis of human interferon-beta-1a with the aim of mapping residues required for activity and receptor binding. The availability of the 3-D crystal structure of human interferon-beta-1a (see Karpusas et al., 1997, Proc. Natl. Acad. Sci. 94: 11813-11818) allows us to identify, for alanine (or serine) substitutions, the solvent-exposed residues available for interferon beta receptor

15   interactions, and to retain amino acids involved in intramolecular bonds. A panel of fifteen alanine scanning mutations were designed that replaced between two and eight residues along distinct regions each of the helices (A, B, C, D, E) and loops (AB1, AB2, AB3, CD1, CD2, DE1, DE2) of interferon-beta-1a. See Example 1.

An amino-terminal histidine tag ("his" tag) was included for affinity purification of

20   mammalian cell expressed mutants (SEQ ID NO: 2:Figure 1). Functional consequences of these mutations were assessed in antiviral and antiproliferation assays. A non-radioactive binding assay was developed to analyze these mutants for their binding to the interferon beta surface cell receptor (IFNAR1/2 cell surface receptor). In addition, an ELISA-based assay employing an IFNAR2- ectodomain/Fc fusion protein to bind

25   interferon was used to map interactions of surfaces between interferon-beta-1a and IFNAR2 (See Example 1). These mutational analyses demonstrated that N- and C- termini lie in a portion of the interferon-beta molecule not important for receptor binding or biological function.

We have identified three types of effects that were caused by targeted mutagenesis.

30   These effects may be advantageous for interferon drug development under certain circumstances. The three types of effect are as follows: (a) mutants with higher antiviral

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activity than that of his-wild-type interferon-beta-1a (e.g. mutant C1); (b) mutants which

display activity in both antiviral and antiproliferation assays, but for which

antiproliferation activity is disproportionately low with respect to antiviral activity,

compared to his-wild-type interferon-beta-1a (e.g., mutants C1, D and DE1); and (c)

5   functional antagonists (e.g., A1, B2, CD2 and DE1), which show antiviral and

antiproliferative activities that are disproportionately low with respect to receptor binding,

compared to his-wild-type interferon-beta-1a.

Moreover, the coupling between the interferon-beta-1a moiety (X) and the second,

non-interferon-beta-1a moiety Z (e.g., an Fc region of an immunoglobulin) can also be

10 effected by any chemical reaction that will bind the two molecules together so long as the

immunoglobulin and the interferon-beta-1a retain their respective activities. This chemical

linkage can include many chemical mechanisms such as covalent binding, affinity binding,

intercalation, coordinate binding and complexation. Representative coupling agents (i.e.,

linkers "Y" in the generic formula) to develop covalent binding between the interferon-

15 beta-1a and immunoglobulin moieties can include organic compounds such as thioesters,

carbodiimides, succinimide esters, diisocyanates such as tolylene-2,6-diisocyanate,

gluteraldehydes, diazobenzenes and hexamethylene diamines such as bis-(p-diazonium-

benzoyl)-ethylenediamine, bifunctional derivatives of imidoesters such as dimethyl

adipimidate, and bis-active fluorine compounds such as 1,5-difluoro-2,4-dinitrobenzene.

20 This listing is not intended to be exhaustive of the various classes of chemical coupling

agents known in the art. Many of these are commercially available such as N-

succinimidyl-3-(2-pyridyldithio) propionate (SPDP), 1-ethyl-3-(3-dimethylamino-propyl)

carbodiimide hydrochloride (EDC); 4-succinimidyloxycarbonyl-alpha-methyl-alpha-(2-

pyridyl-dithio)-toluene (SMPT: Pierce Chem. Co., Cat. # 21558G).

25 IV. UTILITY OF THE INVENTION

The fusion proteins of this invention can be used in therapeutic compositions

whenever interferon beta therapy is called for. These molecules have the normal

advantages associated with fusion proteins, particularly Ig fusions; namely an altered

pharmacokinetics and pharmacodynamics, leading to increased half life and increased

30 residence time in the vasculature. Moreover, the particularly preferred glycosylated

interferon-beta-1a proteins, although similar in structure to interferon beta 1b, are many

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times more biologically active than the non-glycosylated interferon beta 1b. See Runkel et al., 1998, Pharm. Res. 15: 641-649.

The products of the present invention have been found useful in sustaining the half life of therapeutic interferon-beta 1a, and may for example be prepared for therapeutic

5 administration by dissolving in water or acceptable liquid medium. Administration is by either the parenteral, aerosol, or oral route. Fine colloidal suspensions may be prepared for parenteral administration to produce a depot effect, or by the oral route while aerosol formulation may be liquid or dry powder in nature. In the dry, lyophilized state or in solution formulations, the interferon-beta-1a fusions of the present invention should have

10 good storage stability.

The therapeutic proteins of the present invention may be utilized for the prophylaxis or treatment of any condition or disease state for which the interferon-beta-1a constituent is efficacious. In addition, the fusion proteins of the present invention may be utilized in diagnosis of constituents, conditions, or disease states in biological systems or

15 specimens, as well as for diagnosis purposes in non-physiological systems.

In therapeutic usage, the present invention contemplates a method of treating an animal subject having or latently susceptible to such condition(s) or disease state(s) and in need of such treatment, comprising administering to such animal an effective amount of a fusion protein of the present invention which is therapeutically effective for said condition

20 or disease state. Subjects to be treated by the fusions of the present invention include mammalian subjects and most preferably human subjects. Depending on the specific condition or disease state to be combated, animal subjects may be administered interferon-beta-1a fusion proteins of the invention at any suitable therapeutically effective and safe dosage, as may readily be determined within the skill of the art, and without undue

25 experimentation. Because of the species barriers of Type I interferons, it may be necessary to generate interferon-fusion proteins as described herein with interferons from the appropriate species.

The anti-cell proliferative activity of interferon-beta-1a is well known. In particular, certain of the interferon-beta-1a fusions described herein are useful for treating

30 tumors and cancers such as osteogenic sarcoma, lymphoma, acute lymphocytic leukemia, breast carcinoma, melanoma and nasopharyngeal carcinoma, as well as autoimmune

conditions such as fibrosis, lupus and multiple sclerosis. It is further expected that the anti-viral activity exhibited by the fusion proteins, in particular certain of the interferon-beta-1a muteins described herein, may be used in the treatment of viral diseases, such as ECM infection, influenza, and other respiratory tract infections, rabies, and hepatitis. It is also

5   expected that immunomodulatory activities of interferon-beta-1a exhibited by the proteins described herein, may be used in the treatment of autoimmune and inflammatory diseases, such as fibrosis, multiple sclerosis. The ability of interferons to inhibit formation of new blood vessels (angiogenesis or neovascularization) enable proteins of the invention to be used to treat angiogenic diseases such as diabetic retinopathy, retinopathy of prematurity,

10   macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, and Osler-Webber Syndrome. Moreover, the antiendothelial activity of interferon has been known for some time and one potential mechanism of interferon action may be to interfere with endothelial cell activity by inhibiting the production or efficacy of angiogenic factors produced by tumor cells. Some vascular tumors, such as

15   hemangiomas, are particularly sensitive to treatment with interferon. Treatment with interferon-alpha is the only documented treatment for this disease. It is expected that treatment with the interferon-beta-1a fusion proteins of the invention will offer subtantial pharmaceutical benefits in terms of pharmacokinetics and pharmacodynamics, since the conjugate is expected to remain in the vasculature for a longer period of time than non-

20   conjugated interferons, thus leading to more efficient and effective therapy for use as an anti-angiogenic agent. See Example 9.

The polymer-interferon-beta-1a fusions of the invention may be administered per se as well as in the form of pharmaceutically acceptable esters, salts, and other physiologically functional derivatives thereof. In such pharmaceutical and medicament

25   formulations, the interferon-beta-1a preferably is utilized together with one or more pharmaceutically acceptable carrier(s) and optionally any other therapeutic ingredients. The carrier(s) must be pharmaceutically acceptable in the sense of being compatible with the other ingredients of the formulation and not unduly deleterious to the recipient thereof. The interferon-beta-1a is provided in an amount effective to achieve the desired

30   pharmacological effect, as described above, and in a quantity appropriate to achieve the desired daily dose.

The formulations include those suitable for parenteral as well as non-parenteral administration, and specific administration modalities include oral, rectal, buccal, topical, nasal, ophthalmic, subcutaneous, intramuscular, intravenous, transdermal, intrathecal, intra-articular, intra-arterial, sub-arachnoid, bronchial, lymphatic, vaginal, and intra-uterine administration. Formulations suitable for oral, nasal, and parenteral administration are preferred.

When the interferon-beta-1a is utilized in a formulation comprising a liquid solution, the formulation advantageously may be administered orally or parenterally. When the interferon-beta-1a is employed in a liquid suspension formulation or as a powder in a biocompatible carrier formulation, the formulation may be advantageously administered orally, rectally, or bronchially.

When the interferon-beta-1a is utilized directly in the form of a powdered solid, the interferon-beta-1a may advantageously be administered orally. Alternatively, it may be administered nasally or bronchially, via nebulization of the powder in a carrier gas, to form a gaseous dispersion of the powder which is inspired by the patient from a breathing circuit comprising a suitable nebulizer device.

The formulations comprising the proteins of the present invention may conveniently be presented in unit dosage forms and may be prepared by any of the methods well known in the art of pharmacy. Such methods generally include the step of bringing the active ingredient(s) into association with a carrier which constitutes one or more accessory ingredients. Typically, the formulations are prepared by uniformly and intimately bringing the active ingredient(s) into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product into dosage forms of the desired formulation.

Formulations of the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets, tablets, or lozenges, each containing a predetermined amount of the active ingredient as a powder or granules; or a suspension in an aqueous liquor or a non-aqueous liquid, such as a syrup, an elixir, an emulsion, or a draught.

A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared by compressing in a suitable

machine, with the active compound being in a free-flowing form such as a powder or granules which optionally is mixed with a binder, disintegrant, lubricant, inert diluent, surface active agent, or discharging agent. Molded tablets comprised of a mixture of the powdered polymer conjugates with a suitable carrier may be made by molding in a suitable

5   machine.

A syrup may be made by adding the active compound to a concentrated aqueous solution of a sugar, for example sucrose, to which may also be added any accessory ingredient(s). Such accessory ingredient(s) may include flavorings, suitable preservative, agents to retard crystallization of the sugar, and agents to increase the solubility of any

10   other ingredient, such as a polyhydroxy alcohol, for example glycerol or sorbitol.

Formulations suitable for parenteral administration conveniently comprise a sterile aqueous preparation of the active conjugate, which preferably is isotonic with the blood of the recipient (e.g., physiological saline solution). Such formulations may include suspending agents and thickening agents or other microparticulate systems which are

15   designed to target the compound to blood components or one or more organs. The formulations may be presented in unit-dose or multi-dose form.

Nasal spray formulations comprise purified aqueous solutions of the active conjugate with preservative agents and isotonic agents. Such formulations are preferably adjusted to a pH and isotonic state compatible with the nasal mucus membranes.

20   Formulations for rectal administration may be presented as a suppository with a suitable carrier such as cocoa butter, hydrogenated fats, or hydrogenated fatty carboxylic acid.

Ophthalmic formulations such as eye drops are prepared by a similar method to the nasal spray, except that the pH and isotonic factors are preferably adjusted to match that of

25   the eye.

Topical formulations comprise the conjugates of the invention dissolved or suspended in one or more media, such as mineral oil, petroleum, polyhydroxy alcohols, or other bases used for topical pharmaceutical formulations.

In addition to the aforementioned ingredients, the formulations of this invention

30   may further include one or more accessory ingredient(s) selected from diluents, buffers,

flavoring agents, disintegrants, surface active agents, thickeners, lubricants, preservatives (including antioxidants), and the like.

Accordingly, the present invention contemplates the provision of suitable fusion proteins for in vitro stabilization of interferon-beta 1a in solution, as a preferred illustrative
5 application of non-therapeutic application. The fusion proteins may be employed for example to increase the resistance to enzymatic degradation of the interferon-beta 1a. and provides a means of improving shelf life, room temperature stability, and robustness of research reagents and kits.

The following Examples are provided to illustrate the present invention, and should
10 not be construed as limiting thereof. In particular, it will be understood that the in vivo, animal experiments described herein may be varied, so that other modifications and variations of the basic methodology are possible. For example, in Example 7, one of ordinary skill in the art could use other neopterin assays or could alter the number and kind of primate used. These modifications and variations to the Examples are to be regarded as
15 being within the spirit and scope of the invention.

Example 1: Structure/activity studies of human interferon-beta-1a using alanine/serine substitution mutations: Analysis of receptor binding sites and functional domains

A. Overview

20 An extensive mutational analysis of human interferon-beta-1a (IFN-beta-1a) was undertaken with the aims of mapping residues required for activity and receptor binding. The availability of the 3-D crystal structure of human IFN-beta (Karpusas, M. et al. 1997, Proc. Natl. Acad. Sci. 94: 11813-11818) allowed us to identify for alanine (or serine) substitutions the solvent-exposed residues available for receptor interactions, and to retain
25 amino acids involved in intramolecular bonds. A panel of 15 alanine substitution mutations were designed that replaced between 2 and 8 residues along distinct regions of each of the helices (A, B, C, D, E) and loops (AB, CD, DE). An amino-terminal tag consisting of 6 histidine residues was included for affinity purification, as well as an enterokinase linker sequence site for removal of the amino-terminal extension. The
30 resulting interferons are interchangeably referred to as "his tagged-interferon(IFN)-beta" or His_6-interferon-beta" and the like.

Various mutant his tagged-IFN-beta expression plasmids were constructed using a wild type IFN-beta gene construct as a template for mutagenesis. The mutagenesis strategy involved first introducing unique restriction enzyme cleavage sites throughout the wild type his tagged-IFN beta gene, then replacing distinct DNA sequences between the

5   chosen restriction sites with synthetic oligonucleotide duplexes, which encoded the alanine (or serine) substitution mutations. Finally, the mutant IFN genes were subcloned into a plasmid which directed mammalian cell expression in a human 293 kidney cell line.

Functional consequences of these mutations were assessed in antiviral and antiproliferation assays. A non-radioactive IFN binding assay was developed to analyze

10   these mutants in their binding to the surface receptor ("IFNAR1/2 complex") of human Daudi Burkitt's lymphoma cells. In addition, an assay to map interaction surfaces between his-IFN-beta mutants and IFNAR2 was developed that employed a IFNAR2/Fc fusion protein, comprised of the IFN receptor protein IFNAR2 extracellular domain fused to the hinge, CH2 and CH3 domains of human IgG1.

15   1.   **Creation of an interferon beta gene as a template for mutagenesis**

Our strategy to generate IFN-beta alanine (or serine) substituted mutants was to first create a modified IFN-beta gene, which encoded the wild type protein but which carried unique restriction enzyme cleavage sites scattered across the gene. The unique sites were used to exchange wild type sequences for synthetic oligonucleotide duplexes, which

20   encode the mutated codons. In order to obtain an human IFN-beta-1a expression cassette suitable for creation of mutant genes, the IFN-beta cDNA (GenBank accession #E00029) was amplified by PCR. An initial cloning of the IFN-beta gene into plasmid pMJB107, a derivative of pACYC184, see Rose, et. al., 1988, Nucleic Acids Res. 16 (1) 355) was necessary in order to perform site-directed mutagenesis of the gene in a plasmid that lacked

25   the specific restriction sites which would be generated through the mutagenesis.

The PCR primers used to subclone the coding sequences of the human IFN-beta gene also allowed us to introduce an enterokinase linker sequence upstream and in frame with the IFN-beta gene (5' PCR primer 5'TTCTCCGGAGACGATGATGACAAGATGAGCTACAACTT

30   GCTTGGATTCCTACAAAGAAGC-3' (SEQ ID NO: 9: "BET-021", and

3' PCR primer 5'-GCCGCTCGAGTTATCAGTTTCGGAGGTAACCTGTAAGTC-3'

(SEQ ID NO:10: "BET-022") and flanking restriction enzyme sites (BspEI and Xho I)

useful for cloning into plasmid pMJB107 sites. The resulting DNA is refererred to as PCR

fragment A.

5   An efficient signal sequence from the human vascular cell adhesion molecule-1

(VCAM-1) signal sequence and a six histidine tag were introduced into the final construct

from a second DNA fragment created from pDSW247 (fragment B). Plasmid pDSW247 is

a derivative of pCEP4 (Invitrogen, Carlsbad, CA) from which the EBNA-1 gene has been

deleted, and which carries the VCAM-1 signal sequence (VCAMs) fused upstream and in

10   frame with a six histidine tag. The PCR primers that were used to generate the VCAMss- .

1/histidine tag cassette moiety were KID-369 (5' PCR primer 5'-

AGCTTCCGGGGGCCATCATCATCATCATCATAGCT-3': SEQ ID NO: 11) and KID-

421 (3' PCR primer 5'-CCGGAGCTATGATGATGATGATGATGG

CCCCCGGA-3': SEQ ID NO: 12) incorporating flanking restriction enzyme cleavage

15   sites (NotI and BspEI) that allowed excision of the fragment B DNA.

To create a plasmid vector that carried the VCAM-1 signal sequence, his tag and

interferon-beta gene we performed a three-way ligation using gel purified DNA fragments

from plasmid vector pMJB107 (NotI and XhoI cleaved), PCR fragment A (BspEI and

XhoI cleaved) and fragment B (NotI and BspEI cleaved). The ligated plasmid was used to

20   transform either JA221 or XL1-Blue E. coli cells and ampicillin resistant colonies were

picked and tested for inserts by restriction map analysis. Maxiprep DNA was made and the

sequence of the insert was verified by DNA sequencing. The resulting construct was

called pCMG260.

2. Creation of alanine substitution mutants of human interferon-beta in pCMG260

25   The plasmid pCMG260 was used as a template for multiple rounds of mutagenesis

(U.S.E. Site Directed Mutagenesis Kit (Boehringer-Mannheim), which introduced unique

restriction cleavage sites into positions along the IFN-beta protein coding sequence but did

not change the resulting sequence of the protein. The mutagenized plasmids were used to

transform either the JA221 or XL1-Blue strains of E. coli and recombinant colonies

30   selected for chloramphenicol resistance. Chloramphenicol resistant colonies were further

tested for the presence of the desired unique restriction enzyme site by DNA restriction

mapping analysis. The resulting IFN-beta plasmid, pCMG275.8, contained the full set of unique restriction enzyme cleavage sites and the DNA sequence of the gene was verified. The full DNA sequence of the modified, his-tagged interferon beta gene, together with the wild type protein coding sequence, are given in Figure 1.
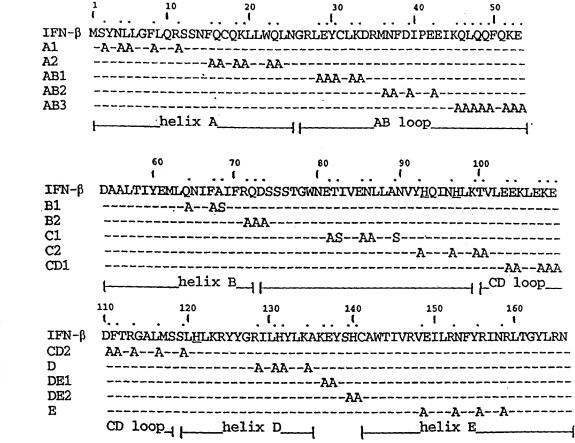
The full set of alanine substitution mutations are depicted in Table 1 (next page). The names of the mutants specify the structural regions (helices and loops) in which the mutations were introduced. The entire panel of alanine (serine) substitutions results in mutation of 65 of the 165 amino acids of human IFN-beta.

The panel of mutants was created from pCMG275.8 by replacing segments of DNA

10   between the unique restriction sites with synthetic oligonucleotide duplexes, which carried the genetic coding information depicted in Table 2 (see below). To create the various alanine substitution mutant plasmids, gel purified pCMG275.8 vector (cleaved with the appropriate restriction enzyme, as indicated on the list below for each IFN-beta structural region) and oligonucleotide duplexes (coding strand sequences are shown in Table 2) were

15   ligated together. The ligation mixtures were used to transform the JA221 strain of E. coli and recombinant colonies selected for ampicillin resistance. Ampicillin resistant colonies were tested for the presence of the insertion of the mutations by screening for appropriate restriction enzyme sites. For two mutants (A2 and CD2), the cloning strategy entailed using two duplexes of synthetic oligonucleotides (shown in Table 2), which carry

20   complementary overhanging ends to allow them to ligate to each other and with the vector-IFN-beta backbone in a three-way ligation. The following list illustrates the sites which were used to clone the mutated oligonucleotides from Table 2. The cloning scheme (subsection B) shows the positions of these unique sites on the interferon beta gene.

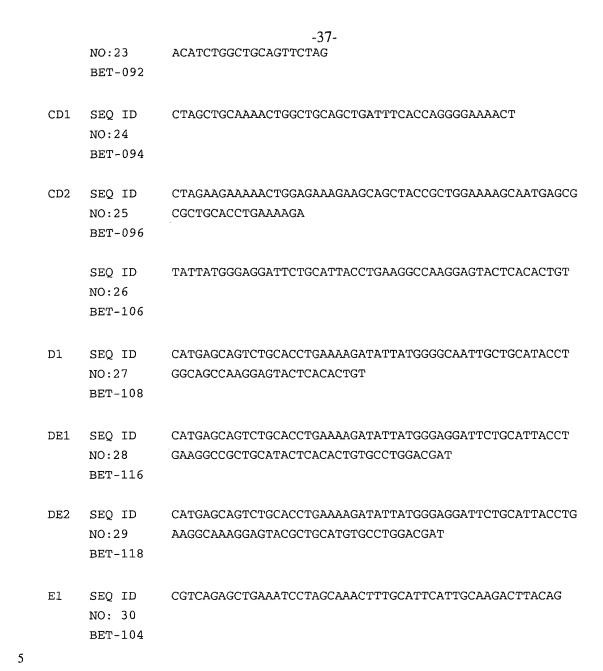|		
	A helix	BspEI to MunI or BglII to Pst I
25	AB loop	MunI to PstI or MunI to BsaHI
	B helix	BspHI to BsaI or BsaHI to BsaI
	C helix	BsaI to XbaI
	CD loop	XbaI to BspHI or XbaI to DraIII
	D helix	BspHI to DraIII
30	DE loop	BspHI to PvuI
	E helix	PvuI to BstEII

Table 1:

Positions of alanine substitution mutations of ᴴᵁIFN-β

```
              1          10         20         30         40         50
              ı    ..  . ı .    .. .ı  ..    .ı. ..  .. .ı .  . ....ı...
IFN-β  MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKE
A1         -A-AA--A--A----------------------------------------
A2         ---------------AA-AA--AA----------------------------
AB1        ---------------:-----------AAA-AA-------------------
AB2        -------------------------------AA-A--A--------------
AB3        ---------------------------------------AAAAA-AAA
           ├──────── helix A ──────────┤├─────── AB loop ─────────┤·


              60         70         80         90         100
              ı    .  .. ı ...    ı ..  .. ı .   . ı  .. ...
IFN-β  DAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKE
B1         -------------A--AS-------------------------------------
B2         ----------------AAA------------------------------------
C1         ------------------------AS--AA--S----------------------
C2         --------------------------------A---A--AA--------------
CD1        ------------------------------------------AA--AAA
           ├───────── helix B ──┤├────────────────────────┤├ CD loop ──


           110        120        130        140        150        160
           ı . .   .  . ı       .  ı ..   . .. ı       . ı  .  .  . ı
IFN-β  DFTRGALMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYRINRLTGYLRN
CD2    AA-A--A--A----------------------------------------------
D          -----------------A-AA--A-----------------------------
DE1        --------------------------AA--------------------------
DE2        ------------------------------AA----------------------
E          -----------------------------------A---A--A--A--------
           CD loop┤├───── helix D ───┤     ├────── helix E ──────────┤
```

The line designated IFN-β shows the wild type human IFN-β
sequence. Alanine or serine substitutions of the IFN-β residues
are shown for each of the mutants and dashes, below relevant
regions, indicate wild type sequences. The helices and loop
structures are indicated as solid lines below the mutants. The
DE loop spans the gap between the D and E helices. Two
additional alanine substitution mutants (H93A, H97A and H121A)
were generated and analyzed in antiviral assays to assess the
effects of mutating these histidines, which chelate zinc in the
crustal structure dimer. Both of these mutants retained full
wild type activity in antiviral assays, suggesting that zinc-
mediated dimer formation is not important for IFN-β activity.

TABLE 2 :

A1	SEQ ID NO:13 BET-053	CCGGAGACGATGATGACAAGATGGCTTACGCCGCTCTTGGAGCCCTACAAG CTTCTAGCAATTTTCAGTGTCAGAAGCTCCTGTGGC
A2	SEQ ID NO:14 BET-039	GATCTAGCAATGCTGCCTGTGCTGCCCTCCTGGCTGCCTTGAATGGGAGGC TTGAATACT
	SEQ ID NO:15 BET-041	GCCTCAAGGACAGGATGAACTTTGACATCCCTGAGGAGATTAAGCAGCTGCA
AB1	SEQ ID NO:16 BET-080	AATTGAATGGGAGGGCTGCAGCTTGCGCTGCAGACAGGATGAACTTTGACAT CCCTGAGGAGATTAAGCAGCTGCA
AB2	SEQ ID NO:17 BET-082	AATTGAATGGGAGGCTTGAATACTGCCTCAAGGACAGGGCTGCATTTGCTAT CCCTGCAGAGATTAAGCAGCTGCA
AB3	SEQ ID NO: 18 BET-084	AATTGAATGGGAGGCTTGAATACTGCCTCAAGGACAGGATGAACTTTGACA
	SEQ ID NO: 19 BET-086	TCCCTGAGGAGATTGCTGCAGCTGCAGCTTTCGCTGCAGCTGA
B1	SEQ ID NO: 20 BET-110	CGCCGCGTTGACCATCTATGAGATGCTCGCTAACATCGCTAGCATTTTCAGA CAAGATTCATCTAGCACTGGCTGGAA
B2	SEQ ID NO: 21 BET-112	CGCCGCATTGACCATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCGCT GCAGCTTCATCTAGCACTGGCTGGAA
C1	SEQ ID NO:22 BET-114	GGAATGCTTCAATTGTTGCTGCACTCCTGAGCAATGTCTATCATCAGATAAA CCATCTGAAGACAGTTCTAG
C2	SEQ ID	GGAATGAGACCATTGTTGAGAACCTCCTGGCTAATGTCGCTCATCAGATAGC

NO:23   ACATCTGGCTGCAGTTCTAG
BET-092

CD1   SEQ ID   CTAGCTGCAAAACTGGCTGCAGCTGATTTCACCAGGGGAAAACT
       NO:24
       BET-094

CD2   SEQ ID   CTAGAAGAAAAACTGGAGAAAGAAGCAGCTACCGCTGGAAAAGCAATGAGCG
       NO:25   CGCTGCACCTGAAAAGA
       BET-096

       SEQ ID   TATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGAGTACTCACACTGT
       NO:26
       BET-106

D1   SEQ ID   CATGAGCAGTCTGCACCTGAAAAGATATTATGGGGCAATTGCTGCATACCT
       NO:27   GGCAGCCAAGGAGTACTCACACTGT
       BET-108

DE1   SEQ ID   CATGAGCAGTCTGCACCTGAAAAGATATTATGGGAGGATTCTGCATTACCT
       NO:28   GAAGGCCGCTGCATACTCACACTGTGCCTGGACGAT
       BET-116

DE2   SEQ ID   CATGAGCAGTCTGCACCTGAAAAGATATTATGGGAGGATTCTGCATTACCTG
       NO:29   AAGGCAAAGGAGTACGCTGCATGTGCCTGGACGAT
       BET-118

E1   SEQ ID   CGTCAGAGCTGAAATCCTAGCAAACTTTGCATTCATTGCAAGACTTACAG
       NO: 30
       BET-104

5

B.   Construction of EBNA 293 expression plasmids

The wild type and mutant IFN-beta genes, fused to the VCAM-1 signal sequence,
his tag and enterokinase linker sequence, were gel purified as 761 base pair NotI and
BamHI restriction fragments.   The purified genes were subcloned into NotI and BamHI
10 cleaved plasmid vector pDSW247, which is a derivative of pCEP4 (Invitrogen, Carlsbad,
CA). Plasmid pDSW247 is an expression vector for transient expression of protein in
human EBNA 293 kidney cells (Invitrogen, Carlsbad, CA). It contains the
cytomegalovirus early gene promoter and EBV regulatory elements which are required for

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high level gene expression in that system, as well as selectable markers for E. coli

(ampicillin resistance) and EBNA 293 cells (hygromycin resistance). The ligated plasmids

were used to transform either JA221 or XL1-Blue E. coli cells and ampicillin resistant

colonies were picked and tested for inserts by restriction map analysis. Maxiprep DNA

5   was made and the sequence of the inserts was verified by DNA sequencing. Positive

clones displaying the desired mutagenized sequences were used to transfect human EBNA

293 kidney cells.

The overall cloning and expression strategy is presented in Figure 12.

C. **Expression and Quantitation of IFN-beta-1a alanine substitution mutants**

10   The human EBNA 293 cells (Invitrogen, Carlsbad, CA, Chittenden, T. (1989) J.

Virol. 63: 3016-3025) were maintained as subconfluent cultures in Dulbecco's Modified

Eagle's media supplemented with 10% fetal bovine serum, 2mM glutamine and 250μg/ml

Geneticin (Life Technologies, Gaithersburg, MD). The pDSW247 expression plasmids

were transiently transfected into EBNA 293 cells using the lipofectamine protocol

15   (Gibco/BRL, Life Technologies). Conditioned media was harvested 3-4 days

posttransfection, cell debris was removed by centrifugation, and the his-IFN-beta

concentration was quantitated by ELISA.

The ELISA assay was performed using polyclonal rabbit antibodies (protein A

purified IgG, antibodies had been raised to purified human IFN-beta-1a) to coat 96-well

20   ELISA plates and a biotinylated form of the same polyclonal rabbit Ig was used as a

secondary reagent to allow interferon detection using streptavidin-linked horseradish

peroxidase (HRP: Jackson ImmunoResearch, W. Grove, PA). A dilution series of

interferon-beta-1a (as AVONEX ® sold by Biogen, Inc.) was used to generate standard

concentration curves. The his-IFN-beta containing conditioned media from the EBNA

25   transfectants were diluted to obtain samples with concentrations ranging between 10ng/ml

and 0.3ng/ml in the ELISA assay. To confirm the concentrations of the IFN-beta in media

determined by ELISA, western blot analysis was performed. Reduced culture supernatants

and IFN-beta-1a standards were subjected to SDS-PAGE on 10-20% gradient gels (Novex,

San Diego, CA) and blotted onto PDVF membranes. Immunoreactive bands were detected

30   with a rabbit polyclonal anti-IFN-beta-1a antiserum (#447, Biogen, Inc., a second

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antiserum that had been raised against IFN-beta-1a), followed by treatment with HRP-linked donkey anti-rabbit IgG (Jackson ImmunoResearch, W. Grove, PA).

D.   Assessing the Interferon-beta Mutants for Receptor Binding

5   The receptor binding properties of the Interferon-beta mutants described in C were assessed using two different binding assays. One assay measured binding of the interferon-beta mutants to a fusion protein, IFNAR2/Fc, comprising the extracellular domain of the human IFNAR2 receptor chain fused to part of the constant region of a human IgG. IFNAR2-Fc was expressed in chinese hamster ovary (CHO) cells and purified

10   by protein A sepharose affinity chromatography according to the instructions of the manufacturer (Pierce Chem. Co., Rockford, IL, catalog #20334). The binding of interferon-beta mutants to IFNAR2-Fc was measured in an ELISA format assay. ELISA plates were prepared by coating flat-bottomed 96 well plates overnight at 4° C with 50 μl/well of mouse anti-human IgG1 monoclonal antibody (CDG5-AA9, Biogen, Inc.) at 10

15   μg/ml in coating buffer (50mM $NaHCO_3$, 0.2mM $MgCl_2$, 0.2mM $CaCl_2$, pH 9.6). Plates were washed twice with PBS containing 0.05% Tween-20, and blocked with 0.5% non-fat dry milk in PBS for 1 hour at room temperature. After two more washes, 50 μl of 1 μg/ml IFNAR2-Fc in 0.5% milk in PBS containing 0.05% Tween-20 was added to each well and incubated for 1 hour at room temperature, and the plates were then washed twice more.

20   Binding of the interferon-beta mutants to IFNAR2-Fc was measured by adding 50 μl/well mutant interferon-beta in conditioned media, serially diluted in Dulbecco's Modified Eagle's Medium (DMEM) supplemented with 10% fetal bovine serum, and incubating for 2 hours at 4 $^\circ$C. Dilutions of interferon-beta mutant typically ranged from approximately 1 μM down to 10 pM. After washing, interferon-beta bound to the plates was detected by

25   adding 50 μl/well of a cocktail consisting of a 1:1000 dilution of a rabbit polyclonal anti-interferon antibody (#447, Biogen, Inc.) plus horseradish peroxidase (HRP)-labelled donkey anti-rabbit IgG (Jackson ImmunoResearch), and incubating for 15 minutes at 4 $^\circ$C. After two washes, HRP substrate was added, and the plate was incubated at 4 $^\circ$C before being read on an ELISA plate reader at an absorbance of 450 nm. Data were plotted as

30   absorbance versus the concentration of mutant interferon-beta, and the affinity for the binding of the mutant interferon-beta to IFNAR2-Fc was determined by fitting the data to a

simple hyperbolic binding equation. Results from these analyses are shown in Figure 3, in which the binding affinity for each mutant, determined in triplicate experiments, is expressed as a percentage of that measured for His_6-wild-type interferon-beta-1a.

5   A second receptor binding assay was used to measure the affinity with which the interferon-beta mutants bound to Daudi cells expressing both receptor chains, IFNAR1 and IFNAR2, which together comprise the receptor for interferon-beta. This FACS-based assay used a blocking monoclonal antibody directed against the extracellular domain of IFNAR1, EA12 (Biogen, Inc.), to distinguish unoccupied (free) receptor from receptor to which interferon-beta was bound. Daudi cells (20 μl at 2.5 x 10^7 cells/ml) were placed in

10   96-well V-bottom ELISA plates, and incubated for 1 hour at 4°C with various concentrations of interferon-beta mutant (20 μl in FACS buffer; 5% FBS, 0.1% NaN_3 in PBS). Desirable serial dilutions of interferon-beta mutants ranged from 0.5 μM down to 0.5 pM. To each well was added 100 ng of biotinylated murine anti-IFNAR1 monoclonal antibody EA12 (10 μl), and the plates incubated for an additional 2 minutes at room

15   temperature before being washed twice with FACS buffer (4°C). The cells were then incubated for 30 minutes at 4°C with 50 μl/well of a 1:200 dilution of R-Phycoerythrin-conjugated streptavidin (Jackson ImmunoResearch, West Grove, PA), washed twice in FACS buffer, resuspended in 300 μl FACS buffer containing 0.5% paraformaldehyde, and transferred into 12x75mm polystyrene tubes (Falcon 2052). The samples were then

20   analyzed by flow cytometry on a FACScan (Becton Dickinson). Data were plotted as mean channel fluorescence intensity (MFCI) versus the concentration of interferon-beta mutant; binding affinities were defined as the concentration of interferon-beta mutant giving 50% inhibition of antibody staining. Each mutant was tested multiple times. Figure 4 shows the receptor binding affinities for each interferon-beta mutant, determined by this

25   method, expressed as a percentage of the affinity measured for His_6-wild-type interferon-beta-1a in each experiment.

E.   Assessing the Interferon-beta Mutants for Function

The interferon-beta mutants were also tested for functional activity using *in vitro* assays for antiviral activity and for the ability of the interferon-beta to inhibit cell

30   proliferation. A minimum of three antiviral assays, each with triplicate data points, were performed on each mutant. His_6-wild-type interferon-beta-1a was included as a reference

in every experiment. The antiviral assays were performed by treating A549 human lung carcinoma cells (ATCC CCL 185) overnight with 2-fold serial dilutions of mutant interferon-beta at concentrations that spanned the range between full antiviral protection and no protection from viral cell killing. The following day, the cells were challenged for

5   two days with encephalomyocarditis virus (ECMV) at a dilution that resulted in complete cell killing in the absence of interferon. Plates were then developed with the metabolic dye MTT (2,3-bis[2-Methoxy-4-nitro-5-sulfo-phenyl]-2H-tetrazolium-5-carboxyanilide) (M-5655, Sigma, St. Louis, MO). A stock solution of MTT was prepared at 5 mg/ml in PBS and sterile filtered, and 50 μl of this solution was diluted into cell cultures (100 μl per

10 well). Following incubation at room temperature for 30 - 60 minutes, the MTT/media solution was discarded, cells were washed with 100 μl PBS, and finally the metabolized dye was solubilized in 100 μl 1.2N hydrochloric acid in 90% isopropanol. Viable cells (as evidenced by the presence of the dye) were quantified by absorbance at 450 nm. Data were analyzed by plotting absorbance against the concentration interferon-beta mutant, and

15 the activity of each mutant was defined as the concentration at which 50% of the cells were killed. Figure 5 shows the activity of each mutant expressed as a percentage of the activity measured for his tagged-wild-type interferon-beta-1a in each experiment.

Interferon-beta mutants were also assessed for function in an antiproliferation assay. Human Daudi Burkitt's lymphoma cells (ATCC # CCL 213) were seeded at 2 x 10^5

20 cells/ml in RPMI 1620 supplemented with 10% defined fetal calf serum (Hyclone, Logan Utah), and 2 mM L-glutamine. Each well also contained a given concentration of interferon-beta mutant in a final total volume of 100 μl of medium per well; the interferon-beta concentrations used were chosen to span the range from maximal inhibition of Daudi cell proliferation to no inhibition (i.e. full proliferation). Duplicate experimental points

25 were used for each concentration of interferon-beta mutant tested, and a duplicate set of untreated cells was included in all experiments. Cells were incubated for two days at 37 °C in 5% CO_2 incubators, after which 1 μCi per well of tritiated thymidine ((methyl-^{3}H) thymidine, Amersham TRK758) in 50 μl medium was added to each well, and incubated for a further 4h. Cells were harvested using a LKB plate harvester, and incorporation of

30 tritiated thymidine was measured using a LKB beta plate reader. Duplicate experimental values were averaged and the standard deviations determined. Data were plotted as mean

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counts per minute versus the concentration of interferon-beta mutant, and the activity of each mutant was defined as the concentration required to give 50% of the maximal observed growth inhibition. Multiple assays for each mutant were performed. Figure 6 shows the results expressed as a percentage of the activity found for his tagged-wild-type

5   interferon-beta-1a in each experiment.

F.   **Properties of the Interferon-Beta Mutants**

Histidine tagged-wild-type interferon-beta-1a was found to have activities in the antiviral and antiproliferation assays that were each about 3-fold lower than the corresponding activities found for untagged wild-type interferon-beta-1a. Because all of

10   the interferon-beta mutants A1-E contain the identical his tag sequence at their N-termini, the effects of the mutations on the properties of the molecule were determined by comparing the activities of these mutants in the antiviral, antiproliferation and binding assays to the activity observed for his tagged-wild-type interferon-beta-1a. In so doing, we assume that variations in the activities of mutants A1-E, compared to his tagged-wild-type

15   interferon-beta-1a, are qualitatively and quantitatively about the same as the effects that these same mutations would have in the absence of the N-terminal his tag. The equivalent assumption for tagged or fusion constructs of other soluble cytokines is commonly held to be true by practitioners of the technique of alanine scanning mutagenesis, especially when the in vitro functional activity of the tagged or fusion construct is close to that of the wild-

20   type cytokine as is the case here. See, for example, Pearce K.H. Jr, et al., *J. Biol. Chem.* 272:20595-20602 (1997) and Jones J.T., et al., J. *Biol. Chem.* 273:11667-11674 (1998)

The data shown in Figures 3-6 suggests three types of effects that were caused by the targeted mutagenesis. These effects may be advantageous for interferon drug development under certain circumstances. The three types of effect are as follows: (a)

25   mutants with higher antiviral activity than that of wild-type interferon-beta-1a (e.g. mutant C1); (b) mutants which display activity in both antiviral and antiproliferation assays, but for which antiproliferation activity is disproportionately low with respect to antiviral activity, compared to wild-type interferon-beta-1a (e.g., mutants C1, D and DE1); and (c) functional antagonists (e.g., A1, B2, CD2 and DE1), which show antiviral and

30   antiproliferative activities that are disproportionately low with respect to receptor binding, compared to wild-type interferon-beta-1a. It can be seen that some mutants fall into more

than one class. These classes are reviewed below. While we have characterized these classes of mutants with respect to those examples listed, it should be appreciated that other mutations in these regions may result in similar, or even enhanced effects on activity:

a) Mutant C1 possesses antiviral activity that is approximately 6-fold greater than that of wild-type his-tagged interferon-beta-1a. This mutant and others of this type are predicted to be useful in reducing the amount of interferon-beta that must be administered to achieve a given level of antiviral effect. Lowering the amount of administered protein is expected to reduce the immunogenicity of the protein and may also reduce side-effects from non-mechanism-based toxicities. Mutations in this class are predicted to be advantageous in situations where the therapeutic benefit of interferon-beta administration results from its antiviral effects, and where antiproliferative effects contribute to toxicity or to unwanted side-effects.

(b) The relative activities (% wild type) of the alanine substituted mutants in antiviral and antiproliferation assay are compared in Figure 7. Coordinately changed activities (i.e. antiviral and antiproliferation activities that differ by the same factor from the activities of the wild-type his tagged-interferon-beta-1a) are seen in most mutants (those lying on the diagonal line). However, several mutants show greater alterations in activity in one assay relative to the other, compared to wild-type his tagged-interferon-beta-1a, as evidenced by displacement from the diagonal. Three such mutants are shown in the Table below. Mutant C1 shows antiviral activity that is ~6-fold higher than that of wild-type his tagged-interferon-beta-1a, but its activity in the antiproliferation assay is similar to that of wild-type. Mutant C1 thus has antiviral activity that is enhanced by a factor of 5.2 over its antiproliferation activity, relative to wild-type his tagged-interferon-beta-1a. Similarly, mutant D displays 65% of wild type activity in the antiviral assay, but only 20% of wild-type activity in the antiproliferation assay, and thus has antiviral activity that is enhanced 3.4-fold over its antiproliferation activity compared to wild type. Mutant DE1 displays 26% of wild type activity in the antiviral assay but only 8.5% in the antiproliferation assay, and thus has antiviral activity that is enhanced 3.0-fold over its antiproliferation activity compared to wild-type his tagged-interferon-beta-1a. When administered at a concentration sufficient to achieve a desired level of antiviral activity, these mutant proteins will show substantially lower levels of antiproliferative activity than

-44-

the wild-type protein. Mutations in this class, like those in class (a), are predicted to be advantageous in situations where the therapeutic benefit of interferon-beta administration results from its antiviral effects, and where antiproliferative effects contribute to toxicity or to unwanted side-effects.

5

Mutant	Antiviral Activity (AV) (% wild type)	Antiproliferative (AP) Activity (% wild type)	AV/AP
C1	571	109	5.2
D	65	19	3.4
DE1	26	8.5	3.0

(c) Mutants with antiviral and antiproliferative activities that are low with respect to receptor binding, as compared to wild-type his tagged-interferon-beta-1a (see Table below). Mutant A1 displays antiviral and antiproliferative activities that are 2.0-fold and

10   1.8-fold higher than that observed for wild-type his tagged-interferon-beta-1a, but binds to the cognate receptor on Daudi cells with an affinity that is 29-fold higher than wild-type. The binding of this mutant to the IFN-beta receptor is thus enhanced approximately 15-fold compared to the antiviral and antproliferation activities of the protein. Similarly, mutants B2, CD2 and DE1 show enhancements of binding over antiviral activity of 4.6-,

15   4.6- and 18-fold, respectively, and over antiproliferation activity of 3.5-, 15- and 54-fold. These proteins are predicted to be useful as functional antagonists of the activity of endogenous IFN-beta, and possibly of other endogenous Type I interferons, because they have the ability to bind to and occupy the receptor, and yet generate only a small fraction of the functional response in the target cells that would be seen with wild type IFN-beta.

Mutant	Antiviral Activity (AV) (% wt)	Antiproliferative Activity (AP) (% wt)	Cell Binding Activity (% wt)	Binding/AV	Binding / AP
A1	200	180	2900	15	16
B2	7.1	9.2	33	4.6	3.5
CD2	150	46	690	4.6	15
DE1	26	8.5	460	18	54

G.   Mutein Relationship to Three Dimensional Structure of Interferon

While published crystal structures for a non-glycosylated form of murine

5   interferon beta (T. Senda, S. Saitoh and Y. Mitsui. Refined Crystal Structure of

Recombinant Murine Interferon-β at 2.15 Å Resolution. *J. Mol. Biol.* **253**: 187-207

(1995)) and for human interferon alpha-2b (R. Radhakrishnan, L.J. Walter, A. Hruza, P.

Reichert, P.P Trotta, T.L. Nagabhushan and M.R. Walter. Zinc Mediated Dimer of Human

Interferon-α2b Revealed by X-ray Crystallography. *Structure.* **4**: 1453-1463 (1996)) had

10   provided models for the polypeptide backbone of human interferon beta, we have recently

solved the structure for interferon-beta-1a in its glycosylated state (M. Karpusas, M. Nolte,

C.B. Benton, W. Meier, W.N. Lipscomb, and S.E Goelz. The Crystal Structure of Human

Interferon-β at 2.2 Å resolution. *Proc. Natl. Acad. Sci.* USA **94**: 11813-11818 (1997)).

The results of our mutational analyses can be summarized with respect to the 3D-

15   structure of interferon-beta-1a (not presented here). Certain mutatations residues created a

reduction in activity (2 to >5 fold reduced). The mutated regions correspond to the substitutions

given in Tables 1 and 2.

Mutations that are most significant in their effect on function resulted in a dramatic

reduction in both activity and cell surface receptor binding. Mutations in this region (A2

20   helix, AB& AB2 loop and E helix) correspond to mutations in the IFNAR2 binding site,

since none of these mutants bound IFNAR/Fc in our assay.

While those mutations that were important for IFNAR2 binding also affected cell

binding, cell surface binding properties are also influenced by residues in other regions of

the molecule (B1 helix, C2 helix). It can be seen in the 3-D models (not shown) depicting the effects of the alanine substitution mutants that the N-terminal, C-terminal and the glycosylated C helix regions of the IFN-beta-1a molecule do not lie within the receptor binding site. Mutations in these regions did not reduce biological activity or reduce cell

5   surface receptor binding.

Example 2: Construction of Plasmids for Expression of Interferon-beta-1a fusion (IFN-beta/Fc) Protein

PCR technology was employed to create an expression plasmid encoding the human IFN-beta DNA sequence fused to the Fc portion of murine IgG2a heavy chain

10   molecule. The plasmid vector pDSW247 (see Example 1) is a derivative of pCEP4 (Invitrogen, Carlsbad, CA), from which the EBNA-1 gene has been deleted. This plasmid was used for the construction of an expression vector useful for transient protein expression in EBNA 293 human kidney cells (Invitrogen, Carlsbad, CA., Shen. E. S., et. al. 1995, Gene 156, 235-239). It was designed to contain a human vascular cell adhesion

15   molecule-I (VCAM-1) signal sequence in frame and upstream of the interferon beta sequence, and an enterokinase linker sequence at the junction of the interferon beta and Ig sequences.

The fusion protein expression cassette was assembled from several DNA fragments. To obtain a DNA fragment encoding the human IFN-beta gene, the cDNA

20   subclone of human IFN-beta (GenBank accession #E00029) was used as a template for PCR using primers (5'- GGTGGTCTCACATGAGCTACAACTTGCTTGGATTCCTACAAGAAGC (SEQ ID NO: 31: "BET-025") and 5'- GCCCTCGAGTCGACCTTGTCATCATCGTCGTTTCGGAGGTAACCTGTAAG (SEQ

25   ID NO: 32: "BET-026") that also incorporated a restriction enzyme cleavage site (BsaI) upstream of the first codon of the IFN-beta. The 3' PCR primer (SEQ ID NO: 32: BET-026) for the IFN-beta gene eliminated the IFN-beta termination codon, and incorporated both an in frame enterokinase linker sequence (DDDDK) and a terminal restriction enzyme site (XhoI), useful for subcloning into the expression vector. The BsaI site

30   introduced upstream of the IFN-beta coding sequence allowed us to ligate the VCAM-1 signal sequence upstream and in frame with the IFN-beta gene coding sequence. This

VCAM-1 signal sequence was also generated by PCR using primer pairs 5'-

CAAGCTTGCTAGCGGCCGCGG-3' (SEQ ID NO: 33: "BET-023" and 5'-

GGTGGTCTCACATGGCTTGAGAAGCTGC-3'(SEQ ID NO: 34: "BET-024") that

contained a 5' restriction enzyme cleavage site (NotI, for ligation onto the pDSW247 NotI

5   cloning site) and a 3' restriction enzyme cleavage site (BsaI, for ligation onto the IFN-beta-

1a 5' PCR fragment). The template for PCR was the human vascular cell adhesion

molecule-1 (VCAM-1) cDNA (GenBank accession number X53051).

To create the IFN-beta-1a/Fc fusion gene the following procedures were

performed. The murine IgG2a fragment was removed from pEAG293 by gel purification

10 of a SalI + BamHI digestion DNA fragment. Plasmsid pEAG293 is a Bluescript IISK+

(Stratagene, LaJolla CA, catalogue #212205) subclone of the hinge, CH2 and CH3

domains of murine IgG2a (GenBank accession number V00798). The PCR primer pairs

5'-AGGTSMARCTGCAGSAGTCW-3' (SEQ ID NO: 35), where S=C or G, M=A or C,

R=A or G, W=A or T, and 5'-CTGAGCTCATTTACCCGGAGTCCGGGA

15 GAAGCTCTT-3' (SEQ ID NO: 36) created flanking SalI and NotI sites at the 5' and 3'

ends of the cassette, respectively. The murine IgG2a Fc domain cassette differs from the

GenBank sequence at a single base (codon V369), creating a silent mutation. Hence, wild

type Fc protein is expressed from this IgG2a Fc cassette.

The DNA fragment containing the VCAM-1 signal sequence fused to the huIFN-

20 beta gene with the C-terminal enterokinase linker sequence, was excised from pCMG258

by a NotI to BamHI digestion and gel purified. The SalI site was present on the original

pDSW247 plasmid, and is located immediately downstream and in frame with the IFN-

beta gene coding sequence. The plasmid vector pDSW247 was prepared as a gel purified

NotI + BamHI fragment (see Example 1). A 3-way ligation was performed, using the

25 above mentioned fragments, to assemble the final expression vector encoding the IFN-

beta-1a/IgG2a fusion. This expression plasmid was named pCMG261 and contains the

VCAM-1 signal sequence in a fusion with the gene for mature human IFN-beta,

enterokinase linker sequence and murine IgG2a Fc domain. The full DNA (SEQ ID NO:1)

and protein sequence (SEQ ID NO:2) of the fusion protein are shown in Figure 2.

30 **Example 3: Production of interferon-beta-1a fusion protein in mammalian cells**

The recombinant IFN-beta/Fc expression vector, pCMG261 was transiently

tranfected into human EBNA 293 kidney cells to achieve expression of an IFN-beta-1a

fusion protein of the invention. This recombinant expression plasmid is transfected by the

lipofectamine protocol (catalogue # 18324-020, Life Techonologies) in EBNA 283 human

5   kidney cells according to the protocol of the manufacturer (Life Technologies,

Gaithersburg, MD, Hawley-Nelson, P., Ciccarone, V., Gebeyehu, G. Jessee, J. , Felgner, P.

L. (1993) Focus 15.73) using 1-3 micrograms plasmid DNA for a 100mm culture dish of

EBNA 293 cells. On the the day following lipofectamine transfection of cells, the media is

replaced with growth media (Dulbecco's modified Eagle's medium, 10% fetal bovine

10   serum, 4mM glutamine, 250 micogram Gentecin/ml (Life Technologies, Gaithersburg,

MD). The conditioned media is harvested 3-4 days later and the concentration of IFN-

beta-1a-Fc was determined as described below.

Production of a IFN-beta/Fc fusion protein in other mammalian cell and

prokaryotic cell expression systems could also be performed upon transfer of the protein

15   coding region for the fusion protein into appropriate expression vectors for those systems.

Alternative expression systems would include mammalian cell expression systems such as

chinese hamster ovary (CHO) cells (Barsoum, J. (1995, Methods in Mol. Biol. 48, chapter

18, 225-237) and NS-0 murine cells (Rossman, C. et al. 1996, Protein Expression and Pur.

7, 335-342), and COS7 green monkey kidney cells (Ettinger, R. et. al. 1996, Proc. Natil.

20   Acad. Sci. USA, 93:23, 13102-13107). Other eukaryotic expression systems that would be

applicable would be the yeast Pichia pastoris (Eldin, P. E. et al. 1997, J. Immun. Methods,

201, 67-75) and Saccharomyces cerevisiae (Horwitz, A. H., 1988,, Proc. Natil. Acad. Sci.

USA, 85, 8678-8682).

Quantitation of the IFN-beta-1a-Fc protein expression levels in the culture

25   supernatants from transfected EBNA 293 cells was performed by ELISA using a protein A

purified IgG fraction of rabbit anti-IFN-beta-1a polyclonal antibodies (the antigen was

purified IFN-beta-1a, Biogen, Inc.) to coat 96-well plates. The antibody detects IFN-beta-

1a standards and culture supernatants in an interferon concentration range between

10ng/mL and 0.3ng/mL. Biotinylated rabbit polyclonal anti-IFN-beta-1a (same antibodies

30   as above) and streptavidin-linked horseradish peroxidase were used to detect bound

interferons. To confirm ELISA values, western blot analysis was performed in which

reduced culture supernatants and IFN-beta-1a standards were run on 5-20% Tris-glycine

gels (Novex, San Diego, CA), transferred to PVDF membrane (Amersham Life Science,

Inc., Cleveland, OH) and detected with a different rabbit polyclonal serum (raised against

IFN-beta-1a), followed by horseradish peroxidase linked-donkey anti-rabbit IgG (Jackson

5   ImmunoResearch, West Grove, PA) antibodies.

Example 4: Antiviral activity of IFN-beta-1a/murine IgG2a fusion protein

Human lung carcinoma cells (A549) were pretreated for 24 hours with IFN-beta-1a

or IFN-beta-murine IgG2a (61, 41, 27, 18, 12, 8.2, 5.5, 3.7, 2.5, 1.6 pg/mL) prior to

challenge with encephalomyocarditis virus (EMCV). Following a two-day incubation with

10   the virus, viable cells were stained with a solution of XTT:PMS (2, 3-bis(2-Methoxy-4-

nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanilide inner salt:Phenazine methosulfate, at

$333\mu g/mL$ and 2ng/mL , respectively, in phosphate buffered saline) and detected by

spectroscopy at 450nM. The assay was performed using triplicate data points for each IFN

concentration.

15   In Figure 8 the standard deviations are shown as error bars. The 50% cytopathic

effect for IFN-beta-1a was determined to be approximately 0.4 pM. The 50% cytopathic

effect for IFN-beta-murine IgG2a was found to be 0.15 pM.

Example 5: Construction and Production of a Human Interferon beta-1a/human

IgG1 Fc Fusion Protein

20   **A.   Construction of Human Interferon beta-1a/human IgG1 Fc Fusion**

Protein

PCR technology was employed to create an expression plasmid encoding the

human IFN beta DNA sequence fused to the Fc portion (hinge, CH2 and CH3 domains) of

the human IgG1 heavy chain molecule.

25   *EBNA construct:* The plasmid vector pCH269 is a derivative of pCEP4 (Invitrogen,

Carlsbad, CA) from which the EBNA-1 gene has been deleted. The plasmid was used for

the construction of an expression vector useful for transient protein expression in EBNA

293 human kidney cells (Invitrogen, Carlsbad, CA; Shen E.S., et.al 1995, Gene 156, 235-

239).

30   The fusion protein expression cassette was assembled from three DNA fragments:

a Not I/ Sal I fragment encoding the VCAM-1 signal sequence in frame and fused to the

sequence encoding human IFN beta, a Sal I/Not I fragment encoding the hinge, CH2 and

CH3 domains of human IgG1, and a Not I fragment of EBNA expression vector pCH269.

Two distinct Not I/Sal I fragments encoding the mature VCAM-1 signal sequence

in frame and fused to the human IFN beta gene were made by PCR technology. The PCR

5   template was plasmid pCMG258 (see Example 2 above) which encodes the mature

VCAM-1 signal sequence in frame and fused to the human IFN beta gene, which itself is

in frame and fused to the enterokinase linker sequence. Two sets of PCR primers were

used. One set of primers (5'- AGCTTGCTAGCGGCCGCGGCCTCACTGGCTTCA-3'

(SEQ ID NO: 37), and 5'- ATACGCGTCGACGTTTCGGAGGTAACATGTAAGTCTG-

10   3': (SEQ ID NO: 38)) introduced an amino acid change from G to C at position 162. This

fragment is called human IFN beta-C162.

The second primer set   (5'-

AGCTTGCTAGCGGCCGCGGCCTCACTGGCTTCA-3'(SEQ ID NO: 39) , and 5'-

TACACGTCGACGCTGCCACCACCGCCGTTTCGGAGGTAACATGTAAGTCTG-3':

15   SEQ ID NO: 40)) also introduced the G162 to C162 amino acid substitution and changed

the enterokinase linker sequence (DDDDK) to a GGGGS linker sequence in frame and

fused 3' to the human IFN beta gene. This fragment is called human IFN beta-C162/G4S.

Both sets of primers contain a 5' Not I site to enable ligation into pCH269, and a 3' Sal I

cleavage site to enable ligation with the Sal I/ Not I fragment of human IgG1.

20   The human IgG1 fragment which encodes the hinge, CH2 and CH3 domains of

human IgG1 was prepared by restriction enzyme (Sal I/ Not I) digestion of plasmid

pEAG409, a derivative of plasmid SAB144 (described in U.S. Patent 5,547,853). The

fragment was excised and gel purified. The EBNA expression vector plasmid pCH269 was

digested with Not I and gel purified.

25   Two human IFN beta-human IgG1 Fc fusion constructs were generated by two

three-way ligations. One construct, called ZL6206 contains the G4S linker; the other

construct, called ZL5107, is a direct fusion. The full DNA and protein sequences of the

open reading frames of the direct fusion (see Figure 10) are shown in SEQ ID NO: 41 and

SEQ ID NO: 42, respectively. The full DNA and protein sequences of the open reading

30   frames of the linker fusion (see Figure 11) are shown in SEQ ID NO: 43 and SEQ ID NO:

44, respectively.

CHO construct:

A human IFN beta-human IgG1 Fc fusion CHO stable expression construct was made which was comprised of the human IFN beta directly linked to human IgG1 Fc. The human IFN beta-human IgG1 Fc fragment was cut from plasmid ZL5107 with Not I and

5   gel purified; it was ligated into the Not I site of pEAG347 (an expression vector containing tandem SV40 early and Adenovirus major late promoters [derived from pAD2beta plasmid], a unique NotI cloning site, followed by SV40 late transcription termination and polyA signals [derived from pCMVbeta plasmid]. pEAG347 contains a pUC19-derived plasmid backbone and a pSV2dhfr-derived dhfr for MTX selection and amplification in

10   transfected CHO cells.).

B.   Production of human interferon-beta-1a/human IgG1 Fc fusion protein in mammalian cells

Transient transfection of human IFN beta fusion constructs into EBNA293 cells:

The recombinant IFN-beta/human IgG1 Fc expression vectors described above

15   were transiently transfected into human EBNA 293 kidney cells to achieve expression of an IFN-beta-1a fusion protein of the invention. These recombinant expression plasmids were transfected by the lipofectamine protocol (catalogue#18324-020, Life Technologies) in EBNA 293 human kidney cells according to the protocol described in Example 3 above. *Stable transfection of human IFN beta-1a/human IgG1 Fc fusion construct (no linker) into*

20   *dhfr- CHO cells:*

The recombinant IFN-beta/human IgG1 Fc (with no linker) dhfr containing expression vector described above was stably transfected into dhfr- CHO cells to achieve expression of an IFN-beta-1a fusion protein of the invention. This recombinant expression plasmid was transfected by electroporation and selection of positive clones was

25   accomplished according the following protocol:

Plasmid DNA (20 mcg) digested with Bgl II was precipitated, resuspended in 800 mcl of HEPES buffer and added to 10×10^7 CHO cells/ml. Following electroporation, cells were cultured in DMEM complete media for 2 days. Cells were then split into 20-40 10 cm dishes with complete DMEM/dialyzed 10% FBS and cultured for 5 days before

30   moving the cells into selection media with escalating (50-200 ng/ml) concentrations of MTX in DMEM for two weeks. At the end of two weeks, single colonies of cells were

selected and expanded. Supernatants derived from 22 CHO clones were tested in antiviral assays.

Activity:

The anti-viral activity of the fusion proteins was determined in CPE assays as described in Example 4. Based on the 60 MU/mg specific activity of the interferon-beta-1a standard used in the assay, the activity of the transiently (EBNA) expressed human interferon-beta-1a/human IgG1 Fc fusion protein with the linker was 900 U/ml and the activity without a linker was 440 U/ml. The activity of CHO expressed human interferon-beta-1a/human IgG1 Fc fusion protein was 50 U/ml.

Example 6: Measurement of interferon-beta-1a antiviral activity in the plasma of mice treated with interferon-beta-1a and interferon-beta-1a/murine IgG2a fusion protein

Mice (C57/B16) are injected i.v. through the tail vein with 50,000 Units of interferon-beta-1a (bulk) or 5,000 Units of interferon-beta-1a-murine IgG2a fusion protein. An equal volume of phosphate buffer is given as a control.

Blood is sampled through retro-orbital bleeds at different time points (immediately, 0.25, 1, 4, 24 and 48 hours) after interferon beta injection. There are at least 3 mice per time point. Whole blood is collected into tubes containing anticoagulant, cells are removed and the resulting plasma frozen until time of assay. The plasma samples are diluted 1:10 into serum free assay media and passed through a 0.2 um syringe filter.

The diluted samples are then titrated into designated wells of a 96 well tissue culture plate containing A549 cells. A standard Interferon-beta-1a (10, 6.7, 4.4, 2.9, 1.3, 0.9 and 0.6 U/ml AVONEX) and 4 samples were run on every plate. The cells are pretreated with samples for 24 hours prior to challenge with EMC virus. Following a two-day incubation with virus, viable cells are stained with a solution of MTT (at 5 mg/ml in phosphate buffer) for 1 hour, washed with phosphate buffer, and solubilized with 1.2 N HCl in isopropanol. The wells were read at 450 nm. Standard curves are generated for each plate and used to determine the amount of interferon-beta-1a activity in each sample. The activity in the samples from the different mice are graphed against the time points in Figure 9.

The slower loss of interferon-beta-1a fusion from circulation as a function of time indicates that the half life of the fusion protein sample is much longer than that of the

unmodified interferon-beta-1a control. A second highly significant finding from the study was that very little of the fusion protein was lost during the distribution phase, as evidenced by the similar high levels of activity at the 15 and 60 minutes timepoints. The data indicate that, unlike the control interferon-beta-1a, the distribution of the interferon-

5   beta-1a fusion protein is largely limited to the vasculature.

Example 7: Comparative Pharmacokinetics and Pharmacodynamics in Primates

Comparative studies are conducted with interferon-beta 1a fusion and native interferon-beta 1a (as non formulated bulk intermediate AVONEX ® interferon-beta-1a in 100 mM sodium phosphate, 200 mM NaCl, pH 7.2) to determine their relative stability and

10   activity in primates. In these studies, the pharmacokinetics and pharmacodynamics of the interferon-beta- 1a fusion in primates is compared to that of native interferon-beta 1a and reasonable inferences can be extended to humans.

Animals and Methods

Study Design

15   This is a parallel group, repeat dose study to evaluate the comparative pharmacokinetics and pharmacodynamics of interferon-beta-1a fusion protein and nonfusion interferon-beta-1a .

Healthy primates (preferably rhesus monkeys) are used for this study. Prior to dosing, all animals will be evaluated for signs of ill health by a Lab Animal Veterinary on

20   two occasions within 14 days prior to test article administration; one evaluation must be within 24 hours prior to the first test article administration. Only healthy animals will receive the test article. Evaluations will include a general physical examination and pre-dose blood draws for baseline clinical pathology and baseline antibody level to interferon-beta-1a. All animals will be weighed and body temperatures will be recorded within 24

25   hours prior to test article administrations.

Twelve subjects are enrolled and assigned to groups of three to receive 1 MU/kg of interferon-beta-1a as either a fused or a non-fused, but otherwise identical interferon-beta-1a. Administration is by either the subcutaneous (SC) or intravenous (IV) routes. Six male animals will receive test article by the IV route (3/treatment) and another 6 male

30   animals will receive test article by the SC route (3/treatment). All animals must be naive

to interferon-beta treatment. Each animal will be dosed on two occasions; doses will be separated by four weeks. The dose volume will be 1.0 mL/kg.

Blood is drawn for pharmacokinetic testing at 0, 0.083, 0.25, 0.5, 1, 1.5, 2, 4, 6, 8, 12, 24, 48, 72, and 96 hours following each injection. Blood samples for measurements of
5   the interferon induced biological response marker, serum neopterin, are drawn at 0, 24, 48, 72, 96, 168, 336, 504 hours following administration of study drug.

Evaluations during the study period include clinical observations performed 30 minutes and 1 hour post-dose for signs of toxicitiy. Daily cageside observations will be performed and general appearance, signs of toxicity, discomfort, and changes in behavior
10   will be recorded. Body weights and body temperatures will be recorded at regular intervals through 21 days post-dose.

Assay Methods

Levels of interferon beta in serum are quantitated using a cytopathic effect (CPE) bioassay. The CPE assay measures levels of interferon-mediated antiviral activity. The
15   level of antiviral activity in a sample reflects the number of molecules of active interferon contained in that sample at the time the blood is drawn. This approach has been the standard method to assess the pharmacokinetics of interferon beta. The CPE assay used in the current study detects the ability of interferon beta to protect human lung carcinoma cells (A549, #CCL-185, ATCC, Rockville, MD) from cytotoxicity due to
20   encephalomyocarditis (EMC) virus. The cells are preincubated for 15 to 20 hours with serum samples to allow the induction and synthesis of interferon inducible proteins that then mount an antiviral response. Afterwards EMC virus is added and incubated for a further 30 hours before assessment of cytotoxicity is made using a crystal violet stain. An internal interferon beta standard as well as an interferon-beta-Ig internal standard is tested
25   concurrently with samples on each assay plate. This standard is calibrated against a natural human fibroblast interferon reference standard (WHO Second International Standard for Interferon, Human Fibroblast, Gb-23-902-53). Each assay plate also includes cell growth control wells containing neither interferon beta of any kind nor EMC, and virus control wells contain cells and EMC but no interferon beta. Control plates containing the standard
30   and samples are also prepared to determine the effect, if any, of the samples on cell growth. These plates are stained without the addition of virus.

Samples and standards are tested in duplicate on each of two replicate assay plates, yielding four data points per sample. The geometric mean concentration of the four replicates is reported. The limit of detection in this assay is 10 units (U)/ml.

Serum concentrations of neopterin are determined at the clinical pharmacology unit

5   using commercially available assays.

Pharmacokinetic and Statistical Methods

RstripTM software (MicroMath, Inc., Salt Lake City, UT) is used to fit data to pharmacokinetic models. Geometric mean concentrations are plotted by time for each group. Since assay results are expressed in dilutions, geometric means are considered

10   more appropriate than arithmetic means. Serum interferon levels are adjusted for baseline values and non-detectable serum concentrations are set to 5 U/ml, which represents one-half the lower limit of detection.

For IV infusion data, a two compartment IV infusion model is fit to the detectable serum concentrations for each subject, and the SC data are fit to a two compartment

15   injection model.

The following pharmacokinetic parameters are calculated:

(i)   observed peak concentration, C_{max} (U/ml);

(ii)   area under the curve from 0 to 48 hours, AUC using the trapezoidal rule;

20   (iii)   elimination half-life;

and, from IV infusion data (if IV is employed):

(iv)   distribution half-life (h);

(v)   clearance (ml/h)

(vi)   apparent volume of distribution, Vd (L).

25   WinNonlin (Version 1.0, Scientific Consulting Inc., Apex, NC) software is used to calculate the elimination half-lives after SC and IM injection.

For neopterin, arithmetic means by time are presented for each group. E_{max}, the maximum change from baseline, is calculated. C_{max}, AUC and E_{max} are submitted to a one-way analysis of variance to compare dosing groups. C_{max} and AUC are

30   logarithmically transformed prior to analysis; geometric means are reported.

Example 8: Anti-Angiogenic Effects of Interferon Beta-1a Fusion

Assessment of the ability of an interferon-beta-1a Fusion to inhibit endothelial cell proliferation in vitro

Human venous endothelial cells (Cell Systems, Cat. # 2V0-P75) and human dermal microvascular endothelial cells (Cell Systems, Cat. # 2M1-C25) are maintained in culture with CS-C Medium Kit (Cell Systems, Cat. # 4Z0-500). Twenty-four hours prior to the experiment, cells are trypsinized, and resuspended in assay medium, 90% M199 and 10% fetal bovine serum (FBS), and are adjusted to desired cell density. Cells are then plated onto gelatin-coated 24 or 96 well plates, either at 12,500 cells/well or 2,000 cells/well, respectively.

After overnight incubation, the assay medium is replaced with fresh medium containing 20 ng/ml of human recombinant basic Fibroblast Growth Factor (Becton Dickinson, Cat. # 40060) and various concentrations of fusion and non-fusion interferon-beta-1a proteins or positive control (endostatin can be used as a positive control, as could an antibody to bFGF). The final volume is adjusted to 0.5 ml in the 24 well plate or 0.2 ml in the 96 well plate.

After seventy-two hours, cells are trypsinized for Coulter counting, frozen for CyQuant fluorescense reading, or labeled with [3H] thymidine.

This in vitro assay tests the human interferon-beta molecules of the invention for effects on endothelial cell proliferation which may be indicative of anti-angiogenic effects in vivo. See O'Reilly, M.S., T. Boehm, Y. Shing, N. Fukal, G. Vasios, W. Lane, E. Flynn, J. Birkhead, B. Olsen, and J. Folkman. (1997). Endostatin: An Endogenous Inhibitor of Angiogensis and Tumor Growth. *Cell* 88, 277-285.

Example 9: In Vivo Model to Test Anti-Angiogenic and Neovascularization Effects of Interferon-beta-1a/ Ig fusion

A variety of models have been developed to test for the anti-angiogenic and anti-neovascularization effects of the molecules described herein. Some of these models have been described in United States Patents 5,733,876 (Mar. 31,1998: "Method of inhibiting angiogenesis) and 5,135,919 (Aug. 4, 1992:" Method and a pharmaceutical composition for the inhibition of angiogenesis "). Other assays include the shell-less chorioallantoic membrane (CAM) assay of S. Taylor and J. Folkman; Nature, 297, 307 (1982) and R.Crum. S.Szabo and J.Folkman; Science. 230. 1375 (1985); the mouse dorsal air sac

method antigiogenesis model of Folkman, J. et al.; J.Exp.Med.,133, 275 (1971) and the rat

corneal micropocket assay of Gimbrone, M.A. Jr. et al., J. Natl. Cancer Inst. 52, 413(1974)

in which corneal vascularization is induced in adult male rats of the Sprague-Dawley

strain (Charles River, Japan) by implanting 500 ng of basic FGF (bovine, R & D Systems,

5   Inc.) impregnated in EVA (ethylene-vinyl acetate copolymer) pellets in each cornea.

Other methods for testing interferon-beta/Ig fusions for anti-angiogenic effects in

an animal model include (but are not limited to) protocols for screening new potential

anticancer agents as described in the original Cancer Chemotherapy Reports, Part 3, Vol.

3, No.2, September 1972 and the supplement In Vivo Cancer Models, 1976-1982, NIH

10   Publication No. 84-2635, February 1984. Because of the species barriers of Type I

interferons, to assess the anti-angiogenic activity of interferon-beta fusions in rodent

models, rodent interferon-beta/:Ig fusion preparations are generated. Such screening

methods are exemplified by a protocol to test for the anti-angiogenic effects of murine

interferon-beta/Ig fusions on subcutaneously-implanted Lewis Lung Carcinoma.

15   *Origin of Tumor Line:*

Arose spontaneously in 1951 as a carcinoma of the lung in a C57BL/6 mouse.

Summary of Test Procedures: A tumor fragment is implanted subcutaneously in the

axillary region of a B6D2F1 mouse. The test agent (i.e, a fusion protein of the invention)

is administered at various doses, subcutaneously (SC) or intraperitoneally (IP) on multiple

20   days following tumor implantation. The parameter measured is median survival time.

Results are expressed as a percentage of control survival time.

Animals:

Propagation: C57BL/6 mice.

Testing: B6D2F1 mice.

25   Weight: Mice should be within a 3 gm weight range with a minimum weight of 18

gm for males and 17 gm for females.

Sex: One sex is used for all test and control animals in one experiment.

Source: One source, if feasible, for all animals in one experiment.

Experiment Size:

30   Ten animals per test group.

Tumor Transfer:

PROPAGATION:

Fragment: Prepare a 2-4 mm fragment of a s.c. donor tumor

Time: Day 13-15

Site: Implant the fragment s.c. in the axillary region with a puncture in the inguinal region.

TESTING:

Fragment: Prepare a 2-4 mm fragment of s.c. donor tumor.

Time: Day 13-15.

Site: Implant the fragment s.c. in the axillary region with a puncture in the inguinal region.

Testing Schedule:

Day 0: Implant tumor. Run bacterial cultures. Test positive control compound in every odd-numbered experiment. Prepare materials. Record deaths daily.

Day 1: Check cultures. Discard experiment if contaminated. Randomize animals. Treat as instructed (on day 1 and on following days).

Day 2: Recheck cultures. Discard experiment if contaminated.

Day 5: Weigh Day 2 and day of initial test agent toxicity evaluation.

Day 14: Control early-death day.

Day 48: Control no-take day.

Day 60: End and evaluate experiment. Examine lungs grossly for tumor.

Quality Control:

Schedule the positive control compound (NSC 26271 (Cytoxan at a dose of 100 mg/kg/injection)) in every odd-numbered experiment, the regimen for which is intraperitoneal on Day 1 only. The lower Test/Control limit for the positive control is 140%. The acceptable untreated control median survival time is 19-35.6 days.

Evaluation:

The parameter measured is median survival time Compute mean animal body weights for Day 1 and Day 5, compute Test/Control ratio for all test groups with . The mean animal body weights for staging day and final evaluation day are computed. The Test/Control ratio is computed for all test groups with > 65 % survivors on Day 5. A

-59-

Test/Control ratio value <86% indicates toxicity. An excessive body weight change difference (test minus control) may also be used in evaluating toxicity.

Criteria for Activity:

An initial Test/Control ratio greater than or equal to 140% is considered necessary to demonstrate moderate activity. A reproducible Test/Control ratio value of greater than or equal to 150% is considered significant activity.